


```
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6632927ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-795-515-5

Query Match 73.4%; Score 445; DB 4; Length 235;
Best Local Similarity 75.0%; Pred. No. 3.le-40;
Matches 87; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 2 IELTQSPAIMASPGKVTMTCSASSSVNMHWFFQOESGTFPKRRIYDTSKLAGVPAFL 61
Db 24 IVLTQSPAIMASPGKVTMTCSASSSVNMHWYQQKSGTSPKRWIYDTSKLAGVPAHF 83

QY 62 SGGSGTFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLELKRADAAPTVSIF 117
Db 84 RGGSGTSYSLTISGMEADAATYYCQQWSSNPFTFGSGTKLEINRADTAPTVSIF 139

RESULT 6
US-09-348-224-5
; Sequence 5, Application US/09348224
; Patent No. 6750325
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda Kay
; APPLICANT: Zivin, Robert Allan
; APPLICANT: Adair, John Robert
; APPLICANT: Athwal, Diljeet Singh
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; FILE REFERENCE: CARP0066
; CURRENT APPLICATION NUMBER: US/09/348,224
; CURRENT FILING DATE: 1999-07-06
; EARLIER APPLICATION NUMBER: 08/116,247
; EARLIER FILING DATE: 1993-09-03
; EARLIER APPLICATION NUMBER: 07/743,377
; EARLIER FILING DATE: 1991-10-04
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 235
; TYPE: PRT
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; ORGANISM: Mouse
US-09-348-224-5

Query Match 73.4%; Score 445; DB 4; Length 235;
Best Local Similarity 75.0%; Pred. No. 3.le-40;
Matches 87; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 2 IELTQSPAIMASPGKVTMTCSASSSVNMHWFFQOESGTFPKRRIYDTSKLAGVPAFL 61
Db 24 IVLTQSPAIMASPGKVTMTCSASSSVNMHWYQQKSGTSPKRWIYDTSKLAGVPAHF 83

QY 62 SGGSGTFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLELKRADAAPTVSIF 117
Db 84 RGGSGTSYSLTISGMEADAATYYCQQWSSNPFTFGSGTKLEINRADTAPTVSIF 139

RESULT 7
US-09-553-498-8
; Sequence 8, Application US/09553498
; Patent No. 6309861
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: Process for the production of naturally folded and secreted protein
; FILE REFERENCE: Case 20379
; CURRENT APPLICATION NUMBER: US/09/553,498
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: EP99107412.1
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 8
; LENGTH: 255
; TYPE: PRT
; ORGANISM: E. coli
;
US-09-553-498-8

Query Match 73.3%; Score 444; DB 3; Length 255;
Best Local Similarity 80.0%; Pred. No. 4.4e-40;
Matches 88; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTMTCSASSSVNMHWFFQOESGTFPKRRIYDTSKLAGVPAFL 60
Db 132 DIELTQSPAIMASPGKVTMTCSASSSVRYMNMWFFQOESGTFPKRRIYDTSKLAGVPAFL 191

QY 61 LSGSGGTFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLELKRADA 110
Db 192 FSGSGGTYSYSLTISMEADAATYYCQQWSSNPFTFGAGTKLELKRADA 241

RESULT 8
US-09-618-869-8
; Sequence 8, Application US/09618869
; Patent No. 6455279
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR CHAPERONES
; TITLE OF INVENTION: CHAPERONES
; FILE REFERENCE: 20381
; CURRENT APPLICATION NUMBER: US/09/618,869
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: EP99114811.5
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 255
; TYPE: PRT
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; ORGANISM: Escherichia coli
US-09-618-869-8

Query Match      73.3%; Score 444; DB 4; Length 255;
Best Local Similarity 80.0%; Pred. No. 4.4e-40;
Matches 88; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTMTCSASSSVNVMHWFQQESGTFPKRRIYDTSKLASGVPAR 60
Db 132 DIELTQSPAIMSASPGKVTMTCSASSSVRYMNVWFQKSGTSPKRWIYDTSKLSGVPAR 191
QY 61 LSGSGSGTEFTLEISRVAEDVGVIYCCQLVEYPLTFGAGTKLELKRAA 110
Db 192 FSGSGSGTSYSLTISMEADAATYCCQWSSNPLTFGAGTKLELKRAA 241

RESULT 9
US-08-737-129A-4
; Sequence 4, Application US/08737129A
; Patent No. 5885816
; GENERAL INFORMATION:
; APPLICANT: Ikuo FUJII et al.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
; TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,129A
; FILING DATE: No. 5885816member 15, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-737-129A-4

Query Match      73.2%; Score 443.5; DB 2; Length 213;
Best Local Similarity 73.5%; Pred. No. 4e-40;
Matches 86; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 1 DIELTQSPAIMSASPGKVTMTCSASSSVNVMHWFQQESGTFPKRRIYDTSKLASGVPAR 60
Db 1 ELVMTQTTPAIMSASPGKVTMTCSASSISYMHWYQQKPGTTPPKRWIYGTSKLTSGVPAR 60
QY 61 LSGSGSGTEFTLEISRVAEDVGVIYCCQLVEYPLTFGAGTKLELKRAAAPTVSIF 117
Db 61 FSGSGSGTSFSLTISMEADAATYCHQRSSYP-TFGGGTKLEIKRAAAPTVSIF 116
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RESULT 10
US-09-171-945-9
; Sequence 9, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-9

Query Match      72.4%; Score 439; DB 3; Length 108;
Best Local Similarity 79.6%; Pred. No. 5.1e-40;
Matches 86; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTMTCSASSSVNVMHWFQQESGTFPKRRIYDTSKLASGVPAR 60
Db 1 DIELTQSPAIMSASPGKVTITCSASSSVTYMHWFQQKPGTSPKLIWYSTSNLASGVPAR 60
QY 61 LSGSGSGTEFTLEISRVAEDVGVIYCCQLVEYPLTFGAGTKLELKRA 108
Db 61 FSGSGSGTSYSLTISRMEADAATYCCQQRSTYPLTFGAGTKLELKRA 108
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RESULT 11
US-09-526-738A-2
; Sequence 2, Application US/09526738A
; Patent No. 6630584
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DVELOPMENT
; APPLICANT: LTD.
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336
; CURRENT APPLICATION NUMBER: US/09/526,738A
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Huananus
US-09-526-738A-2

Query Match      70.5%; Score 427; DB 4; Length 256;
Best Local Similarity 73.7%; Pred. No. 3e-38;
Matches 84; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTMTCSASSSVNVMHWFQQESGTFPKRRIYDTSKLASGVPAR 60
Db 132 DIELTQSPAIMSASPGKVTITCSASSSVNVMHWFQQKPGTSPKLIWISSTSNLASGVPAR 191
QY 61 LSGSGSGTEFTLEISRVAEDVGVIYCCQLVEYPLTFGAGTKLELKRAAAPT 114
Db 192 FSGSGSGTSYSLTISRMEADAATYCCQRRSSYPYTFGGGTKLQIKRAAAGAPV 245
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Wed Oct 13 13:59:33 2004

RESULT 12
US-09-526-738A-4
; Sequence 4, Application US/09526738A
; Patent No. 6630584
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
; APPLICANT: LTD.
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336
; CURRENT APPLICATION NUMBER: US/09/526,738A
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Humanus
US-09-526-738A-4

Query Match 70.5%; Score 427; DB 4; Length 258;
Best Local Similarity 73.7%; Pred. No. 3.1e-38;
Matches 84; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

Qy 1 DIETQSPAIMSASPGKVTMTCSASSSVNYMHWFQQESGTFPKRRIYDTSKLAGVVPAR 60
Db 134 DIETQSPAIMSASPGKVTITCSASSSVNYMHWFQQKPGTSPKLTWISSTSNLAGVVPAR 193

Qy 61 LSGSGSGTFTLEISRKAEDVGVYCCQLVEYPLTFGAGTKLELKRAAPTV 114
Db 194 FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPYTFGGGTLQIKRAAGAPV 247

RESULT 13
US-08-652-507-2
; Sequence 2, Application US/08652507
; Patent No. 5876691
; GENERAL INFORMATION:
; APPLICANT: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN
; TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderrhye, P.C.
; STREET: 1100 No. 5876691th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,507
; FILING DATE: 02-Jul-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Arthur R. Crawford
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 117-211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-507-2

Query Match 70.3%; Score 426; DB 2; Length 270;
Best Local Similarity 79.0%; Pred. No. 4.2e-38;
Matches 83; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 4 LTQSPAIMSASPGKVTMTCSASSSVNYMHWFQQESGTFPKRRIYDTSKLAGVVPARLSG 63
Db 165 LTQSPAIMSASPGKVTITCSASSSVNYMHWFQQKPGTSPKLTWISSTSNLAGVVPARFSG 224

Qy 64 SSGSGTFTLEISRKAEDVGVYCCQLVEYPLTFGAGTKLELKRA 108
Db 225 SSGSGTSYSLTISRMEADAATYYCQQRSSYPYTFGGGTLQIKRAAGAPV 247

RESULT 14
US-08-661-052-16
; Sequence 16, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-661-052-16

Query Match 70.3%; Score 426; DB 2; Length 553;
Best Local Similarity 79.0%; Pred. No. 1e-37;
Matches 83; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 4 LTQSPAIMSASPGKVTMTCSASSSVNYMHWFQQESGTFPKRRIYDTSKLAGVVPARLSG 63
Db 415 LTQSPAIMSASPGKVTITCSASSSVNYMHWFQQKPGTSPKLTWISSTSNLAGVVPARFSG 474

Qy 64 SSGSGTFTLEISRKAEDVGVYCCQLVEYPLTFGAGTKLELKRA 108
Db 475 SSGSGTSYSLTISRMEADAATYYCQQRSSYPYTFGGGTLQIKRAAGAPV 247

RESULT 15

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US-09-188-082-16
; Sequence 16, Application US/09188082
; Patent No. 6270765
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/188,082
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-188-082-16

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		Query Match	70.3%;	Score 426;	DB 3;	Length 553;	
		Best Local Similarity	79.0%;	Pred. No. 1e-37;			
		Matches 83; Conservative	7;	Mismatches 15;	Indels 0;	Gaps 0;	
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Qy	64	SGSGTEFTLEISRVAEDVGVIYCQOLVEYPLTFAGTKLELKRA	108				
Dd	475	SGSGTSYSLTIISNMEADAATYYCQQRSSVPLTFAGTKLELKRA	519				

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Job time : 30.2625 secs

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OM nucleic - protein search, using frame_plus_n2p model
Run on: October 13, 2004, 13:12:35 ; Search time 21.8705 Seconds
(without alignments)
2201.453 Million cell updates/sec

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Perfect score: 673
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 956278

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosam62 -TRANS=human40.cdi
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	538	79.9	222	2	US-08-190-199A-67
2	538	79.9	235	2	US-08-190-199A-61
3	535.5	79.6	120	2	US-08-652-558-38
4	535	79.5	119	2	US-08-752-844-16
5	535	79.5	119	2	US-08-591-196-16
6	535	79.5	119	4	US-09-293-533-16
7	531.5	79.0	140	3	US-08-943-136-4
8	531.5	79.0	140	3	US-08-973-518-4
9	529.5	78.7	242	6	5455030-15
10	525.5	78.1	121	3	US-08-881-037-67
11	523	77.7	119	1	US-08-667-769A-15
12	523	77.7	119	5	PCT-US95-17082A-15

13	521.5	77.5	112	3	US-09-189-129-3	Sequence 3, Appli
14	521.5	77.5	112	4	US-09-824-286-3	Sequence 3, Appli
15	517.5	76.9	239	2	US-08-860-174A-2	Sequence 2, Appli
16	515	76.5	119	3	US-08-483-749A-14	Sequence 14, Appli
17	512.5	76.2	137	2	US-08-621-751A-4	Sequence 4, Appli
18	507.5	75.4	239	6	5455030-13	Patent No. 5455030
19	505.5	75.1	241	4	US-09-554-765-13	Sequence 13, Appli
20	499.5	74.2	116	3	US-08-397-411-4	Sequence 4, Appli
21	498.5	74.1	272	4	US-08-756-416-39	Sequence 39, Appli
22	498	74.0	113	2	US-08-606-293-2	Sequence 2, Appli
23	489	72.7	111	1	US-08-467-420A-15	Sequence 15, Appli
24	489	72.7	111	1	US-08-470-110A-15	Sequence 15, Appli
25	489	72.7	111	2	US-08-940-371-15	Sequence 15, Appli
26	489	72.7	111	3	US-08-637-647-15	Sequence 15, Appli
27	488	72.5	115	3	US-08-881-037-22	Sequence 22, Appli
28	484	71.9	97	3	US-08-881-037-66	Sequence 66, Appli
29	478	71.0	113	2	US-08-606-293-6	Sequence 6, Appli
30	476	70.7	152	2	US-08-752-844-4	Sequence 4, Appli
31	476	70.7	152	2	US-08-591-196-4	Sequence 4, Appli
32	476	70.7	152	3	US-09-192-838B-4	Sequence 4, Appli
33	476	70.7	152	4	US-09-293-533-4	Sequence 4, Appli
34	476	70.7	152	4	US-09-324-191-4	Sequence 4, Appli
35	476	70.7	263	2	US-08-752-844-66	Sequence 66, Appli
36	476	70.7	263	4	US-09-293-533-66	Sequence 66, Appli
37	473.5	70.4	120	2	US-08-652-558-8	Sequence 8, Appli
38	473.5	70.4	120	3	US-09-254-189-5	Sequence 5, Appli
39	473	70.3	107	1	US-08-122-546-12	Sequence 12, Appli
40	473	70.3	107	2	US-08-764-938-12	Sequence 12, Appli
41	473	70.3	107	3	US-09-131-052-12	Sequence 12, Appli
42	473	70.3	107	3	US-09-131-053A-12	Sequence 12, Appli
43	472	70.1	264	3	US-08-564-164A-4	Sequence 4, Appli
44	471.5	70.1	107	1	US-07-942-245-14	Sequence 14, Appli
45	469.5	69.8	215	4	US-09-170-769A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-190-199A-67
; Sequence 67, Application US/08190199A
; Patent No. 5830663
; GENERAL INFORMATION:
; APPLICANT: EMBLETON, Michael J.
; APPLICANT: GOROCOV, Guy
; APPLICANT: JONES, Peter T.
; APPLICANT: WINTER, Gregory P.
; TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY MADISON & SUTRO, L.I.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,199A
; FILING DATE: 13-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/01483
; FILING DATE: 10-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9212419.7
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9117352.6
; FILING DATE: 10-AUG-1991

; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-190-199A-67

Alignment Scores:
Pred. No.: 1.62e-59 Length: 222
Score: 538.00 Matches: 104
Percent Similarity: 87.60% Conservative: 2
Best Local Similarity: 85.95% Mismatches: 7
Query Match: 79.94% Indels: 8
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x US-08-190-199A-67 (1-222)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGTCTCTGGGATTTCATTAAACAGATATGGTGTACACTGGGTTCGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
QY 121 CCAGGAAAGGCTCTGGAGTGGCTGGGAGTAATATGGACTGGTGAAGCACAAATATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCCAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspArgGly 100
QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGCGCAAGGACCAAGGTACCGTCTCC 360
Db 101 Ala-----TyrTrpGlyGlnGlyThrLeuValThrValSer 112
QY 361 TCA 363
Db 113 Ala 113

RESULT 2

US-08-190-199A-61
; Sequence 61, Application US/08190199A
; Patent No. 5830663
; GENERAL INFORMATION:
; APPLICANT: EMBLETON, Michael J.
; APPLICANT: GOROCHOV, Guy
; APPLICANT: JONES, Peter T.
; APPLICANT: WINTER, Gregory P.
; TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,199A
; FILING DATE: 13-JUL-1994
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/01483
; FILING DATE: 10-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9212419.7
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9117352.6
; FILING DATE: 10-AUG-1991
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-190-199A-61

Alignment Scores:
Pred. No.: 1.66e-59 Length: 235
Score: 538.00 Matches: 104
Percent Similarity: 87.60% Conservative: 2
Best Local Similarity: 85.95% Mismatches: 7
Query Match: 79.94% Indels: 8
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x US-08-190-199A-61 (1-235)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGTCTCTGGGATTTCATTAAACAGATATGGTGTACACTGGGTTCGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
QY 121 CCAGGAAAGGCTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCACAAATATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCCAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspArgGly 100
QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGCGCAAGGACCAAGGTACCGTCTCC 360
Db 101 Ala-----TyrTrpGlyGlnGlyThrLeuValThrValSer 112
QY 361 TCA 363
Db 113 Ala 113

RESULT 3

US-08-652-558-38
; Sequence 38, Application US/08652558
; Patent No. 5861155
; GENERAL INFORMATION:
; APPLICANT: LIN, AUGUSTINE YEE-THARN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF
; STREET: 75 STATE STREET, 23RD FLOOR
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,558
; FILING DATE: JUNE 6, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB94/00387
; FILING DATE: NOVEMBER 21, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, LEON R.
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,497-L
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-558-38

Alignment Scores:
Pred. No.: 2.6e-59 Length: 120
Score: 535.50 Matches: 104
Percent Similarity: 90.91% Conservative: 6
Best Local Similarity: 85.95% Mismatches: 10
Query Match: 79.57% Indels: 1
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x US-08-652-558-38 (1-120)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
|||
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20

QY 61 ACTTGCACTGTCTCTGGGATTTCATTAAACAGATATGGTGTACACTGGGTTGCCAGCCT 120
|||
Db 21 ThrCysThrValSerGlyPheSerLeuThrAlaTyrGlyValAsnTrpValArgGlnPro 40

QY 121 CCAGGAAAGGGTCTGGAGTGGTGGGAGTAATATGGACTGGTGGGAGCACAACAAATTATAAT 180
|||
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyMetIleTrpGlyAspGlyAsnThrAspTyrAsn 60

QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAAGAGCCAAAGTTTCTTA 240
|||
Db 61 SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80

QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
|||
Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaArgTyrTyrCysAlaArgAspVal 100

QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCAGGGACACGGTCACCGTCTCC 360
|||
Db 101 Thr---AlaThrLeuTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrValSer 119

QY 361 TCA 363
|||
Db 120 Ser 120

RESULT 4

US-08-752-844-16
; Sequence 16, Application US/08752844
; Patent No. 5935821
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA

; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-752-844-16

Alignment Scores:

Pred. No.: 2.99e-59 Length: 119
Score: 535.00 Matches: 104
Percent Similarity: 88.43% Conservative: 3
Best Local Similarity: 85.95% Mismatches: 12
Query Match: 79.49% Indels: 2
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x US-08-752-844-16 (1-119)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
|||
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20

QY 61 ACTTGCACTGTCTCTGGGATTTCATTAAACAGATATGGTGTACACTGGGTTGCCAGCCT 120
|||
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40

QY 121 CCAGGAAAGGGTCTGGAGTGGTGGGAGTAATATGGACTGGTGGGAGCACAACAAATTATAAT 180
|||
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpGlyAspGlySerThrAsnTyrAsn 60

QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAAGAGCCAAAGTTTCTTA 240
|||
Db 61 SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80

QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
|||
Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaArgTyrTyrCysAlaArgGlu***** 100

QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCAGGGACACCGTCAACCGTCTCC 360
|||
Db 101 *****TyrTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrValSer 118

QY 361 TCA 363
|||
Db 119 Ser 119

RESULT 5

QY	121	CCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCACAATAATTATAAT	181
Db	41	ProGlyLysGlyLeuGlnTrpLeuGlyValIleTrpGlyAspGlySerThrAsnTyrAsn	60
QY	181	TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAAGAGCCAAAGTTTCTTA	240
Db	61	SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu	80
QY	241	AAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT	300
Db	81	LysMetAsnSerLeuGlnThrAspThrAlaArgTyrCysAlaArgGlu*****	100
QY	301	ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCC	360
Db	101	***-----**TyrTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrValSer	118
QY	361	TCA 363	
Db	119	Ser 119	

RESULT 7
 US-08-943-136-4
 ; Sequence 4, Application US/08943136
 ; Patent No. 6291208
 ; GENERAL INFORMATION:
 ; APPLICANT: Anand, Naveen N
 ; APPLICANT: Barber, Brian H
 ; APPLICANT: Cates, George A
 ; APPLICANT: Caterini, Judith E
 ; APPLICANT: Klein, Michel H
 ; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
 ; TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sim & McBurney
 ; STREET: 6th Floor, 330 University Avenue
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5G 1R7
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/943,136
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/483,576
 ; FILING DATE: 07-JUNE-1995
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Stewart, Michael I
 ; REGISTRATION NUMBER: 24,973
 ; REFERENCE/DOCKET NUMBER: 1038-733
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 595-1155
 ; TELEFAX: (416) 595-1163
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 140 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-943-136-4

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Query Match:      78.97% Indels:      1
DB:              3       Gaps:        1

US-10-049-868A-2 (1-363) x US-08-943-136-4 (1-140)

QY    1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCTGGTGCGCCCTCACAGAGCCCTGTCCATC 60
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db    21 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 40

QY    61 ACTTGCACTGTCTCTGGGATTTCATTAAACAGATATGGTGTTACACTGGGTTGCCAGCCT 120
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db    41 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 60

QY    121 CCAGGAAGGGTCTGGAGTGGCTGGGAGTAATAATATGGACTGGTGGAGCACAAAATTATAAT 180
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db    61 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerIleAsnTyrAsn 80

QY    181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACCTCCAAGAGCCAAAGTTTTCTTA 240
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db    81 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnPheLysSerGlnValPheLeu 100

QY    241 AAAATGAACAGTCTGCAGACTGATGACACAGCCCATGTACTACTGTGCCAGAGATCGATCT 300
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db    101 LysMetSerSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAlaTyrGly 120

QY    301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCAAGGGACCACGGTCAACGCTCTCC 360
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db    121 AspTyrVal--HisTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrAlaSer 139

QY    361 TCA 363
      |||
Db    140 Ser 140

RESULT 8
US-08-973-518-4
; Sequence 4, Application US/08973518
; Patent No. 6328962
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; APPLICANT: Barber, Brian H
; APPLICANT: Cates, George A
; APPLICANT: Caterini, Judith E
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,518
; FILING DATE: 07-APR-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-973-518-4
Alignment Scores:
Pred. No.: 8.92e-59 Length: 140
Score: 531.50 Matches: 103
Percent Similarity: 88.43% Conservative: 4
Best Local Similarity: 85.12% Mismatches: 13
Query Match: 78.97% Indels: 1
DB: 3 Gaps: 1

US-10-049-868A-2 (1-363) x US-08-973-518-4 (1-140)
QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCTGGCGCCCTCACAGAGCCCTGTCCATC 60
Db 21 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 40
QY 61 ACTTGCACTGTCTCTGGGATTTTCATTAAACAGATATGGTGACACTGGGTTCCGCCAGCCT 120
Db 41 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 60
QY 121 CCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGAAGCACAAATTATAAT 180
Db 61 ProGlyLysGlyLeuGlnTrpLeuGlyValIleTrpAlaGlyGlySerIleAsnTyrAsn 80
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCAAAGTTTCTTA 240
Db 81 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnPheLysSerGlnValPheLeu 100
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGCTACTGTGCCAGAGATCGATCT 300
Db 101 LysMetSerSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAlaTyrGly 120
QY 301 ACTATGATTACGGCTATGCTATGGACTACTGGGGCCCAAGGACCACGGTCACCGTCTCC 360
Db 121 AspTyrVal---HisTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrAlaSer 139
QY 361 TCA 363
Db 140 Ser 140

RESULT 9
5455030-15
; Patent No. 5455030
; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
; POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/40,440
; FILING DATE: 1-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
; SEQ ID NO:15:
; LENGTH: 242
5455030-15
Alignment Scores:
Pred. No.: 2.02e-58 Length: 242
Score: 529.50 Matches: 103
Percent Similarity: 90.00% Conservative: 5
Best Local Similarity: 85.83% Mismatches: 11
Query Match: 78.68% Indels: 1
DB: 6 Gaps: 1
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US-10-049-868A-2 (1-363) x 5455030-15 (1-242)
QY 4 GTGCAGCTGCAGGAGTCTGGACCTGGCTGGCGCCCTCACAGAGCCCTGTCCATCACT 63
Db 124 ValGlnLeuLysGluSerGlyProValLeuValAlaProSerGlnSerLeuSerIleThr 143
QY 64 TGCACCTGTCTCTGGGATTTTCATTAAACAGATATGGTGACACTGGGTTCCGCCAGCCTCCA 123
Db 144 CysThrValSerGlyPheSerLeuThrAsnTyrGlyValHisTrpValArgGlnProPro 163
QY 124 GGAAGGGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGAAGCACAAATTATAATTCG 183
Db 164 GlyLysGlyLeuGlnTrpLeuGlyValIleTrpAlaGlyGlyAsnThrAsnTyrAsnSer 183
QY 184 GCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCCAAGTTTCTTAAAA 243
Db 184 AlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeuLys 203
QY 244 ATGAACAGTCTGCAGACTGATGACACAGCCATGCTACTGTGCCAGAGATCGATCTACT 303
Db 204 MetAsnSerLeuGlnIleAspAspThrAlaIleTyrTyrCysAlaLys---ArgLeuGlu 222
QY 304 ATGATTACGGCTATGCTATGGACTACTGGGGCCCAAGGACCACGGTCACCGTCTCCTCA 363
Db 223 ArgIlePheTyrTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 242

RESULT 10
US-08-881-037-67
; Sequence 67, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Glick, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Konski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-881-037-67
Alignment Scores:
Pred. No.: 4.84e-58 Length: 121
```

Score: 525.50 Matches: 104
Percent Similarity: 87.60% Conservative: 2
Best Local Similarity: 85.95% Mismatches: 14
Query Match: 78.08% Indels: 1
DB: 3 Gaps: 1

US-10-049-868A-2 (1-363) x US-08-881-037-67 (1-121)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
|||||
Db 1 GlnValGlnLeuLeuGluSerGlyProValLeuValAlaProSerGlnSerLeuSerIle 20
61 ACTTGCACTGCTCTGGGATTTCATTAAACAGATATGGTGTAACAGACTGGGTTCCGCCAGCCT 120
|||||
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
121 CCAGGAAAGGTCCTGGAGTGGTGGGAGTAATATGGACTGGTGAAGCACAAATTATAAT 180
|||||
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60
181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAAGAGCCAAAGTTTCTTA 240
|||||
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
|||||
Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaLysHisLeuPro 100
301 ---ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCCAAGGACCAACGGTCACCGTC 357
|||||
Db 101 TyrGlyAsnTyrGlyTyrTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrVal 120
358 TCC 360
|||
Db 121 Ser 121

RESULT 11

US-08-667-769A-15
; Sequence 15, Application US/08667769A
; Patent No. 5783184
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,769A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17082
; FILING DATE: 22-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470110

; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-667-769A-15

Alignment Scores:
Pred. No.: 9.98e-58 Length: 119
Score: 523.00 Matches: 100
Percent Similarity: 88.43% Conservative: 7
Best Local Similarity: 82.64% Mismatches: 12
Query Match: 77.71% Indels: 2
DB: 1 Gaps: 1

US-10-049-868A-2 (1-363) x US-08-667-769A-15 (1-119)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
|||||
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
61 ACTTGCACTGCTCTGGGATTTCATTAAACAGATATGGTGTAACAGACTGGGTTCCGCCAGCCT 120
|||||
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrSerValHisTrpValArgGlnPro 40
121 CCAGGAAAGGTCCTGGAGTGGTGGGAGTAATATGGACTGGTGAAGCACAAATTATAAT 180
|||||
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaSerGlyGlyThrAspTyrAsn 60
181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAAGAGCCAAAGTTTCTTA 240
|||||
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
|||||
Db 81 LysLeuAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspProPro 100
301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCCAAGGACCAACGGTCACCGTCCTCC 360
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Db 101 SerSerLeu-----LeuArgLeuAspTyrTrpGlyGlnGlyThrThrLeuThrValSer 118
361 TCA 363
|||
Db 119 Ser 119

RESULT 12

PCT-US95-17082A-15
; Sequence 15, Application PC/TUS9517082A
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.

; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17082A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-17082A-15

Alignment Scores:
Pred. No.: 9.98e-58 Length: 119
Score: 523.00 Matches: 100
Percent Similarity: 88.43% Conservative: 7
Best Local Similarity: 82.64% Mismatches: 12
Query Match: 77.71% Indels: 2
DB: 5 Gaps: 1

US-10-049-868A-2 (1-363) x PCT-US95-17082A-15 (1-119)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20

QY 61 ACTTGCACTGTCTCTGGATTTCATTAACAGATATGGTGTACACTGGGTTCCGACGCTT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrSerValHisTrpValArgGlnPro 40

QY 121 CCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGGAGCACAATAATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaSerGlyGlyThrAspTyrAsn 60

QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAAGAGCCCAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80

QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCCATGTACTACTGTGCCAGAGATCGATCT 300
Db 81 LysLeuAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAspProPro 100

QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCCAAGGACCACGGTCACCGTCTCC 360
Db 101 SerSerLeu-----LeuArgLeuAspTyrTrpGlyGlnGlyThrThrLeuThrValSer 118
QY 361 TCA 363
Db 119 Ser 119

RESULT 13
US-09-189-129-3
; Sequence 3, Application US/09189129
; Patent No. 6323027
; GENERAL INFORMATION:
; APPLICANT: Burkly, Linda C
; APPLICANT: Benjamin, Christopher D
; APPLICANT: Hession, Catherine A
; APPLICANT: Whitty, Adrian
; TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/189,129
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: A006 PCT CIP
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 60/017,466
; FILING DATE: 10-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A006 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 679-2000
; TELEFAX: 617 679-2838
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-189-129-3

Alignment Scores:
Pred. No.: 1.51e-57 Length: 112
Score: 521.50 Matches: 98
Percent Similarity: 92.17% Conservative: 8
Best Local Similarity: 85.22% Mismatches: 6
Query Match: 77.49% Indels: 3
DB: 3 Gaps: 1

US-10-049-868A-2 (1-363) x US-09-189-129-3 (1-112)

QY 10 CTGCAGGAGTCTGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCATTGCACT 69
Db 1 LeuGlnGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIleThrCysThr 20
QY 70 GTCTCTGGGATTTCATTAACAGATATGGTGTACACTGGGTTCCGAGCCTCCAGGAAAG 129

Db 21 ValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnProProGlyLys 40

QY 130 GGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCACAAATTATAATTCGGCTCTC 189
|||||
Db 41 GlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsnSerAlaLeu 60
|||||

QY 190 ATGTCAGACTGAGCATCAGCAAGACAACACTCCAAGAGCCAAAGTTTCTTAAAAATGAAC 249
|||||
Db 61 MetSerArgLeuAsnIleAsnArgAspAsnSerLysSerGlnIlePheLeuLysMetAsn 80
|||||

QY 250 AGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCTACTATGATT 309
|||||
Db 81 SerLeuGlnThrAspAspThrAlaIleTyrTyrCysAlaArgGluGlySerThrVal--- 99
|||||

QY 310 ACGGCCTATGCTATGGACTACTGGGGCCCAAGGGACCAACGGTCACC 354
:::|
Db 100 -----AspSerMetAspTyrTrpGlyGlnGlyThrValThr 112
:::|

RESULT 14

US-09-824-286-3
; Sequence 3, Application US/09824286
; Patent No. 6770745
; GENERAL INFORMATION:
; APPLICANT: Burkly, Linda C
; Benjamin, Christopher D
; Hession, Catherine A
; Whitty, Adrian
; TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/824,286
; FILING DATE: 02-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,466
; FILING DATE: 10-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A006 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 679-2000
; TELEFAX: 617 679-2838
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-824-286-3

Alignment Scores:

Pred. No.:	1.51e-57	Length:	112
Score:	521.50	Matches:	98
Percent Similarity:	92.17%	Conservative:	8
Best Local Similarity:	85.22%	Mismatches:	6
Query Match:	77.49%	Indels:	3
DB:	4	Gaps:	1

US-10-049-868A-2 (1-363) x US-09-824-286-3 (1-112)

QY 10 CTGCAGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCCATCACTTGCACT 69
|||||

Db 1 LeuGlnGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIleThrCysThr 20
|||||

QY 70 GTCTCTGGGATTTCAATTAAACAGATATGGTGTACACTGGGTTTCGCCAGCCTCCAGGAAAG 129
|||||

Db 21 ValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnProProGlyLys 40
|||||

QY 130 GGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGGAAGCACAAATTATAATTCGGCTCTC 189
|||||

Db 41 GlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsnSerAlaLeu 60
|||||

QY 190 ATGTCAGACTGAGCATCAGCAAGACAACACTCCAAGAGCCAAAGTTTCTTAAAAATGAAC 249
|||||

Db 61 MetSerArgLeuAsnIleAsnArgAspAsnSerLysSerGlnIlePheLeuLysMetAsn 80
|||||

QY 250 AGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCTACTATGATT 309
|||||

Db 81 SerLeuGlnThrAspAspThrAlaIleTyrTyrCysAlaArgGluGlySerThrVal--- 99
|||||

QY 310 ACGGCCTATGCTATGGACTACTGGGGCCCAAGGGACCAACGGTCACC 354
:::|

Db 100 -----AspSerMetAspTyrTrpGlyGlnGlyThrValThr 112
:::|

RESULT 15

US-08-860-174A-2
; Sequence 2, Application US/08860174A
; Patent No. 5989830
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Paul James
; APPLICANT: VAN DER LOGT, Cornelis Paul Erik
; APPLICANT: VERHOEIJEN, Martine Elisa
; APPLICANT: WILSON, Steve
; TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
; TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; STREET: 9th Floor, East Tower
; CITY: WASHINGTON, D.C.
; STATE:
; COUNTRY: UNITED STATES
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text
; SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,174A
; FILING DATE: June 16, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95307332.7
; FILING DATE: October 16, 1995
; APPLICATION NUMBER: PCT/EP/96/03605
; FILING DATE: August 14, 1996
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-860-174A-2

Alignment Scores:

Pred. No.:	6.69e-57	Length:	239
Score:	517.50	Matches:	100
Percent Similarity:	87.60%	Conservative:	6
Best Local Similarity:	82.64%	Mismatches:	10

Query Match:	76.89%	Indels:	5
DB:	2	Gaps:	1
US-10-049-868A-2 (1-363) x US-08-860-174A-2 (1-239)			
QY	1	CAGGTGCAGCTGCAGGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCCATC	60
Db	124	GlnValGlnLeuGlnGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle	143
QY	61	ACTTGCACTGTCTCTGGGATTTTCATTAAACAGATATGGTGTAACACTGGGTGCGCCAGCCT	120
Db	144	ThrCysThrValSerGlyPheSerLeuThrGlyTyrGlyValAsnTrpValArgGlnPro	163
QY	121	CCAGGAAAGGGTCTGCAGTGGCTGGGAGTATATGGACTGGTGGAGCGCAAAATTATAAT	180
Db	164	ProGlyLysGlyLeuGluTrpLeuGlyMetIleTrpGlyAspGlyAsnThrAspTyrAsn	183
QY	181	TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAGAGCCCAAGTTTCTTA	240
Db	184	SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu	203
QY	241	AAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCACAGATCGATCT	300
Db	204	LysMetAsnSerLeuHisThrAspAspThrAlaArgTyrTyrCysAlaArgGluArgAsp	223
QY	301	ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCCAAGGGACCACGGTCACCGTCTCC	360
Db	224	-----TyrArgLeuAspTyrTrpGlyGlnGlyThrThrValThrValSer	238
QY	361	TCA	363
Db	239	Ser	239

Search completed: October 13, 2004, 13:31:12
Job time : 22.8705 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 13, 2004, 13:12:25 ; Search time 21.3809 Seconds
(without alignments)
3231.093 Million cell updates/sec

Title: US-10-049-868A-1
Perfect score: 674
Sequence: 1 gacattgagctcaccagtc.....gtatccatttcaagcttcc 359

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/US10049868/runat_13102004_132817_24805/app_query.fasta_1.1038
-DB=PIR_79 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10049868@CGN_1_1_77@runat_13102004_132817_24805 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length DB ID	Description	

1	460	68.2	235 2 S25058	Ig kappa chain - m	
2	448	66.5	140 2 PL0013	Ig kappa chain pre	
3	437	64.8	107 2 PC4405	Ig kappa chain v r	
4	427	63.4	130 1 JL0079	Ig kappa chain pre	
5	422	62.6	106 2 B54378	Ig light chain v r	
6	422	62.6	107 2 A30562	Ig kappa chain v r	
7	420	62.3	107 2 PD0011	Ig kappa chain v r	
8	419	62.2	103 2 S29591	Ig kappa chain v r	
9	419	62.2	132 2 S05268	Ig kappa chain pre	
10	417	61.9	106 2 PS0071	Ig kappa chain v r	
11	417	61.9	107 2 B30562	Ig kappa chain v r	
12	416	61.7	106 2 G27887	Ig kappa chain v r	
13	415	61.6	104 2 B49049	Ig kappa chain v r	
14	413	61.3	107 2 S11119	Ig kappa chain v r	

15	411	61.0	107 2 S11118	Ig kappa chain v r
16	405	60.1	107 2 S11121	Ig kappa chain v r
17	402.5	59.7	108 2 G30560	Ig kappa chain v r
18	401	59.5	107 2 PT0406	Ig kappa chain v r
19	400	59.3	107 2 PT0403	Ig light chain v r
20	399	59.2	107 2 S11112	Ig kappa chain v r
21	398	59.1	107 2 S11117	Ig kappa chain v r
22	396	58.8	107 2 PT0398	Ig light chain v r
23	394	58.5	104 2 JC6076	anti-D-dimer monoc
24	392	58.2	107 2 PT0402	Ig light chain v r
25	390	57.9	100 2 S29590	Ig kappa chain v r
26	389.5	57.8	106 2 S11114	Ig kappa chain v r
27	389	57.7	130 2 H32456	Ig kappa chain pre
28	386	57.3	107 2 PT0401	Ig light chain v r
29	385	57.1	106 2 PS0070	Ig kappa chain v r
30	385	57.1	120 2 A34871	Ig kappa chain v r
31	384	57.0	97 2 PH1084	Ig light chain v r
32	384	57.0	107 2 S11113	Ig kappa chain v r
33	384	57.0	107 2 PT0395	Ig light chain v r
34	384	57.0	130 2 S04573	Ig kappa chain pre
35	382	56.7	97 2 S26341	Ig light chain v r
36	382	56.7	107 2 S11116	Ig kappa chain v r
37	382	56.7	107 2 PT0400	Ig light chain v r
38	382	56.7	107 2 A42848	Ig light chain v r
39	380	56.4	107 2 S11123	Ig kappa chain v r
40	379	56.2	107 1 KVMSX4	Ig kappa chain v r
41	376.5	55.9	145 2 PL0014	Ig kappa chain pre
42	376	55.8	105 2 S26338	Ig kappa chain v r
43	376	55.8	107 2 PT0397	Ig light chain v r
44	376	55.8	130 2 A32513	Ig kappa chain pre
45	373	55.3	120 2 S66536	Ig light chain v r

ALIGNMENTS

RESULT 1
S25058

Ig kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C;Accession: S25058
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific
A;Reference number: S25057
A;Accession: S25058
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-235 <FIS>
A;Cross-references: EMBL:X67211; NID:G54828; PIDN:CAA47650.1; PID:G54829
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;38-111/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 2.29e-35 Length: 235
Score: 460.00 Matches: 92
Percent Similarity: 85.34% Conservative: 7
Best Local Similarity: 79.31% Mismatches: 17
Query Match: 68.25% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x S25058 (1-235)

QY	4	ATTGAGCTCACCCAGTCTCCAGCAATCATGTGTGCATCTCCAGGGGAGAGGTCACCATG	63
Db	24	IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGlnLysValThrMet	43
QY	64	ACCTGCAGTGCACGTTCAAGTGTTAATTACATGCACCTGGTTCACGACGAGGATCGGGCACC	123
Db	44	ThrCysSerAlaSerSerValSerLysMetGlnTrpTyrGlnGlnLysSerGlyThr	63
QY	124	TTCCCCAAAAGAGGATTTATGACACATCCAAACTGGCTTCTTGAGTGCCTGCTGCCTC	183

D b	64	SerProLysArgT <i>r</i> PileTyrAspThrSerLysLeuAlaSerGlyValProGlyArgPhe	83
Q Y	184	AGTGGCAGTGGGTCTGGGACAGAAATTCACCCCTGGAAATCAGTAGAGTGAGGTGAGGAT	243
D b	84	SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGluAsp	103
Q Y	244	GTGGGTGTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTCCGGTGGTGGGACC	303
D b	104	AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGlyThr	123
Q Y	304	AACTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC	351
D b	124	LysLeuGluLeuLysArqAlaAspAlaAlaProThrValSerIlePhe	139

RESULT 2
PL0013
Ig kappa chain precursor V region (4C11) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C/Accession: PL0013
R/Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A/Title: Structural basis of stimulatory anti-idiotypic antibodies.
A/Reference number: PL0011; MUID:88142863; PMID:3125424
A/Accession: PL0013
A/Molecule type: mRNA
A/Residues: 1-140 <CHE>
A/Experimental source: cell line 4C11
C/Comment: This protein is an anti-idiotypic antibody that induces an anti-
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-22/Domain: signal sequence #status predicted <SIG>
F/23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
F/38-111/Domain: immunoglobulin homology <IMM>
F/46-55/Region: complementarity-determining 1
F/71-77/Region: complementarity-determining 2
F/110-118/Region: complementarity-determining 3
F/130-140/Domain: constant region (fragment) #status predicted <COR>

Alignment Scores:		
Pred. No.:	3.22e-34	140
Score:	448.00	88
Percent Similarity:	82.76%	Matches: 8
Best Local Similarity:	75.86%	Conservative: 20
Query Match:	66.47%	Mismatches: 0
DB:	2	Indels: 0
		Gaps: 0
US-10-049-868A-1 (1-359) x	PL0013	(1-140)

[illegible]

RESULT 3
PC4405
Ig kappa
C;Specie
C;Date:
C;Access

IG kappa chain V region (F3, anti-AFP) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 10-Nov-1997 #sequence_revision 23-Jan-1998 #text_change
 C/Accession: PC4405
 R/Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
 Chinese Biochem. J. 12, 648-653, 1996
 A/Title: Generation of a phage display library of the immunoglobulin
 A/Reference number: PC4405
 A/Accession: PC4405
 A/Molecule type: mRNA
 A/Residues: 1-107 <DEN>
 A/Cross-references: UNIPROT:Q8K1F0
 A/Experimental source: spleen cell
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 F;16-89/Domain: immunoglobulin homology <INM>

Alignment Scores:			
Pred. No.:	3.57e-33	Length:	107
Score:	437.00	Matches:	84
Percent Similarity:	86.92%	Conservative:	9
Best Local Similarity:	78.50%	Mismatches:	14
Query Match:	64.84%	Indels:	0
	2	Gaps:	0
DB:			

US-10-049-868A-1 (1-359) x PC4405 (1-107)

QY		1	GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCAACC	60
Db		1	AspileGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr	20
QY		61	ATGACCTGCAGTGCCAGTTCAAAGTGTTAATTACATGCACACTGGTTCACAGCAGGAGTCGGGC	120
Db		21	MetThrCysSerAlaSerSerIleSerTyrMetHisTrpTyrGlnGlnLysProGly	40
QY		121	ACCTTCCCCAAAAGAAGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC	180
Db		41	ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArg	60
QY		181	CTCAGTGGCAGTGGGTCTGGGACAGAATTCCACCCCTGGAATCAGTAGAGTGAAGGCTGAG	240
Db		61	PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerArgValGluAlaGlu	80
QY		241	GATGTGGGTGTGATTACTGTCAACAACCTTGTAGAGTATCCGCTCAGTTCGGTGCTGGG	300
Db		81	AspAlaAlaThrTyrTyrCysGlnGlnTrpArgAspAsnProProThrPheGlyGlyGly	100
QY		301	ACCAAGCTGGAGCTGAACGG	321
Db		101	ThrLysLeuGluIleLysArg	107

```

RESULT 4
JL0079
Ig kappa chain precursor V region (anti-phenylloxazalone 6F6) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1991 #sequence revision 09-Aug-1996 #text_change 16-Jul-1999
C/Accession: JL0079; A49044; E49044
R/Kaartinen, M.; Rocca-Serra, J.; Maekelae, O.
Mol. Immunol. 25, 859-865, 1988
A/Title: Combinatorial association of V genes: one VH gene codes for three
A/Reference number: JL0076; UID:89Q96973; PMID:3211160

```

A;Cross-references: GB:M27792; NID:G197159
A;Experimental source: mRNA clones for anti-phenylloxazalone antibody 6F6
A;Note: the authors translated the codon TTC for residue 8 as Pro and TTC for
A;Note: the codon given for 1-Met (AGT) is inconsistent with the authors' tri
R;Milstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E.
Eur. J. Immunol. 22, 1627-1634, 1992
A;Title: Non-random features of the repertoire expressed by the members of c
A;Reference number: A49044; MUID:92289826; PMID:1601044

A;Accession: A49044
A;Molecule type: DNA
A;Residues: 1-25 <MIL>
A;Cross-references: GB:S37663; NID:g250214; PIDN:AAB22331.1; PID:g250217
A;Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBIP:106809)
A;Accession: B49044
A;Molecule type: DNA
A;Residues: 114-116 <MIL2>
A;Cross-references: GB:S37664; NID:g250215; PIDN:AAB22332.1; PID:g250218
A;Experimental source: BALB/c germ-line
A;Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 additional disulfide bonds.
C;Genetics:
A;Gene: V(kappa)Ox1
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>
F;38-111/Domain: immunoglobulin homology <IMM>
F;45-109/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 3.07e-32 Length: 130
Score: 427.00 Matches: 84
Percent Similarity: 85.05% Conservative: 7
Best Local Similarity: 78.50% Mismatches: 16
Query Match: 63.35% Indels: 0
DB: 1 Gaps: 0

US-10-049-868A-1 (1-359) x JL0079 (1-130)

QY 4 ATTGAGCTCAGCTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATG 63
||| |||||
Db 24 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43

QY 64 ACTGCAGTGCAGTTCAAGTGTTAATTACATGCACCTGGTTCAGCAGGAGTCGGGCACC 123
|||||
Db 44 ThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGlyThr 63

QY 124 TTCCCCAAAAGAGGATTTATGACACATCCAACTGGCTTCGGAGTCCCTGCTCGCCTC 183
|||||
Db 64 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArgPhe 83

QY 184 AGTGGCAGTGGGTCTGGGACAGAATTACCCCTGGAATCAGTAGAGTGAAGGCTGAGGAT 243
|||||
Db 84 SerGlySerGlySerGly***SerTyrSerLeuThrIleSerSerMetGluAlaGluAsp 103

QY 244 GTGGGTGTATTACTGTCAACAACCTTGATAGAGTATCCGCTCAGCTTCGGTTCGGGCACC 303
|||||
Db 104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGlyThr 123

QY 304 AAGCTGGAGCTGAAACGGGCT 324
|||||
Db 124 LysLeuGlu**LysArgAla 130

RESULT 5
B54378
Ig light chain V region anti-triplex DNA - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B54378
R;Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.
J. Biol. Chem. 269, 7019-7023, 1994
A;Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluorescently labeled DNA.
A;Reference number: A54378; MUID:94165109; PMID:7509814
A;Accession: B54378
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <AGA>
A;Cross-references: GB:S68985; NID:g545746; PIDN:AAB30096.1; PID:g545747

A;Experimental source: spleen and myeloma cell line MOPC 315.43
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBIP:144175)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 9.22e-32 Length: 106
Score: 422.00 Matches: 82
Percent Similarity: 85.71% Conservative: 8
Best Local Similarity: 78.10% Mismatches: 15
Query Match: 62.61% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x B54378 (1-106)

QY 4 ATTGAGCTCAGCTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATG 63
||| |||||
Db 2 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrIle 21

QY 64 ACCTGCAGTGCAGTTCAAGTGTTAATTACATGCACCTGGTTCAGCAGGAGTCGGGCACC 123
|||||
Db 22 ThrCysSerAlaSerSerValSerTyrMetHisTrpPheGlnGlnLysProGlyThr 41

QY 124 TTCCCCAAAAGAGGATTTATGACACATCCAACTGGCTTCGGAGTCCCTGCTCGCCTC 183
|||||
Db 42 SerProLysLeuTrpIleTyrSerThrSerLysLeuAlaSerGlyValProAlaArgPhe 61

QY 184 ACTGGCAGTGGGTCTGGGACAGAATTACCCCTGGAATCAGTAGAGTGAAGGCTGAGGAT 243
|||||
Db 62 SerGlySerGlySerGlyThrSerTyrSerLeuProIleSerArgMetGluAlaGluAsp 81

QY 244 GTGGGTGTATTACTGTCAACAACCTTGATAGAGTATCCGCTCAGCTTCGGTTCGGGCACC 303
|||||
Db 82 AlaAlaThrTyrTyrCysGlnGlnArgSerSerTyrProIleThrPheGlyAlaGlyThr 101

QY 304 AAGCTGGAGCTGAAA 318
|||||
Db 102 LysLeuGluLeuLys 106

RESULT 6
A30562
Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C;Accession: A30562
R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.
J. Immunol. 142, 888-893, 1989
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-binding site.
A;Reference number: A30562; MUID:89110066; PMID:2464031
A;Accession: A30562
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <SIK>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 9.21e-32 Length: 107
Score: 422.00 Matches: 82
Percent Similarity: 84.91% Conservative: 8
Best Local Similarity: 77.36% Mismatches: 16
Query Match: 62.61% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x A30562 (1-107)

QY 4 ATTGAGCTCAGCTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATG 63
||| |||||
Db 2 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 21

QY 64 ACCTGCAGTGCCAGTCAAGTGTTAATTACATGCACTGGTTCCAGCAGGAGTCGGGCACC 123
Db 22 ThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGlyThr 41
QY 124 TTCCCCAAAGAGGATTATGACACATCCAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db 42 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArgPhe 61
QY 184 AGTGGCAGTGGTCTGGACAGAATTCCACCTGGAAATCAGTAGACTGAAGGTGAGGAT 243
Db 62 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGluAsp 81
QY 244 GTGGGTGTGATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTCCGGTGGTGGACC 303
Db 82 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProTyrThrPheGlyGlyGlyThr 101
QY 304 AAGCTGGAGCTGAAACGG 321
Db 102 LysLeuGluIleLysArg 107

RESULT 7
PD0011

Ig kappa chain V region (VLB10, anti-AFP) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 21-Jan-2000
C;Accession: PD0011
R;Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
Chinese Biochem. J. 12, 648-653, 1996
A;Title: Generation of a phage display library of the immunoglobulin repertoire from hum
A;Reference number: PC4405
A;Contents: Spleen
A;Accession: PD0011
A;Molecule type: mRNA
A;Residues: 1-107 <DEN>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-89/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 1.42e-31 Length: 107
Score: 420.00 Matches: 82
Percent Similarity: 85.98% Conservative: 10
Best Local Similarity: 76.64% Mismatches: 15
Query Match: 62.31% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x PD0011 (1-107)

QY 1 GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCACC 60
Db 1 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20
QY 61 ATGACCTGCAGTGCCAGTTCAAAGTGTAAATTACATGCACTGGTTCCAGCAGGAGTCGGGC 120
Db 21 MetThrCysSerAlaSerSerIleSerTyrMetHisTrpTyrGlnGlnLysProGly 40
QY 121 ACCTTCCCCAAAGAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 41 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaLys 60
QY 181 CTCAGTGGCAGTGGTCTGGACAGAATTCCACCTGGAAATCAGTAGACTGAAGGTGAG 240
Db 61 GlySerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerArgValGluAlaGlu 80
QY 241 GATGTGGGTGTGATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTCCGTGGTGGG 300
Db 81 AspAlaAlaThrTyrTyrCysGlnGlnTrpArgAspAsnProProThrProGlyGlyGly 100
QY 301 ACCAAGCTGGAGCTGAAACGG 321
Db 101 ThrLysLeuGluIleLysArg 107

RESULT 8
S29591

Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S29591
R;Kavaler, J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Accession: S29591
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-103 <KAV>
A;Cross-references: EMBL:X59094; NID:g52227; PIDN:CAA41820.1; PID:g52228
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-88/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 1.77e-31 Length: 103
Score: 419.00 Matches: 82
Percent Similarity: 86.41% Conservative: 7
Best Local Similarity: 79.61% Mismatches: 14
Query Match: 62.17% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x S29591 (1-103)

QY 4 ATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCACCATG 63
Db 1 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 20
QY 64 ACCTGCAGTGCCAGTTCAAAGTGTAAATTACATGCACTGGTTCCAGCAGGAGTCGGGCACC 123
Db 21 ThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGlyThr 40
QY 124 TTCCCCAAAGAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db 41 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArgPhe 60
QY 184 AGTGGCAGTGGTCTGGACAGAATTCCACCTGGAAATCAGTAGACTGAAGGTGAGGAT 243
Db 61 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGluAsp 80
QY 244 GTGGGTGTGATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTCCGTGGTGGGACC 303
Db 81 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGlyThr 100
QY 304 AAGCTGGAG 312
Db 101 LysLeuGlu 103

RESULT 9
S05268

Ig kappa chain precursor V-J region (38C13-V1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
C;Accession: S05268; J10062; S03846
R;Levy, S.
submitted to the EMBL Data Library, February 1989
A;Reference number: S05267
A;Accession: S05268
A;Molecule type: mRNA
A;Residues: 1-132 <LEV>
A;Cross-references: EMBL:X14098; NID:g52562; PIDN:CAA32260.1; PID:g736261
R;Carroll, W.L.; Starnes, C.O.; Levy, R.; Levy, S.
J. Exp. Med. 168, 1607-1620, 1988
A;Title: Alternative V kappa gene rearrangements in a murine B cell lymphoma. An expl
A;Reference number: J10061; MUID:89035985; PMID:3141553
A;Accession: J10062
A;Molecule type: mRNA
A;Residues: 1-120 <CAR>
A;Cross-references: EMBL:X14098
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin


```

Db      62 SerGly**Gly**GlyThrSerTyrSerLeuThrIleSerSerMetPheAlaGluAsp 81
      244 GTGGGTGTGTTACTGTCAACAACCTTGTAGAGTATCCGCTCAGCTTCGGTGGTGGACC 303
      82 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGlyThr 101
      304 AAGCTGGAGCTGAAACGG 321
      102 LysLeuGluLeuLysArg 107

RESULT 15
S11118
Ig kappa chain V region (clone NQ5-61.1.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C;Accession: S11118
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A;Reference number: S07331; MUID:83271467; PMID:6877353
A;Accession: S11118
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <KAA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-89/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:      9.99e-31      Length:      107
Score:          411.00      Matches:      82
Percent Similarity: 83.02%      Conservative: 6
Best Local Similarity: 77.36%      Mismatches: 18
Query Match:     60.98%      Indels:      0
DB:              2          Gaps:      0

US-10-049-868A-1 (1-359) x S11118 (1-107)

QY      4 ATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGTCAACCATG 63
Db      2 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 21
      64 ACCTGCAGTCCAGTCAAGTGTTAATTACATGCACTGGTTCAGCAGGAGTCGGGCACC 123
      22 ThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGlyThr 41
      124 TTCCCCAAAAGAGGATTTATGACACATCCAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
      42 SerProLysArgTrpIleTyrAspThrSerLysLeuAspSerGlyValProAlaArgPhe 61
      184 AGTGGCAGTGGGTCTGGGACAGAAATTCACCCCTGGAATCAGTAGAGTGAAAGCTGAGGAT 243
      62 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetPheAlaGluAsp 81
      244 GTGGGTGTGTTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTTCGGTGGTGGACC 303
      82 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGlyThr 101
      304 AAGCTGGAGCTGAAACGG 321
      102 LysLeu**Leu***Arg 107
```

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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 13, 2004, 13:01:14 ; Search time 103.175 Seconds
(without alignments)
4004.053 Million cell updates/sec

Title: US-10-049-868A-1
Perfect score: 674
Sequence: 1 gacattgagtcaccagtc.....gtatccatcttcaagcttcc 359

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 3650362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10049868/runat_13102004_132817_24791/app_query.fasta_1.1038
-DB=UniProt_02 -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10049868 @CGN_1_1_305@runat_13102004_132817_24791 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	452	67.1	112	2	Q8K1F2 mus musculu
2	451	66.9	235	2	Q91W12 mus musculu
3	444	65.9	134	2	Q8VDD0 mus musculu
4	433	64.2	112	2	Q8K1F0 mus musculu
5	421	62.5	107	1	KV6F MOUSE
6	419	62.2	112	2	Q8K1F3 mus musculu
7	419	62.2	114	2	Q8K1F1 mus musculu
8	416	61.7	107	1	KV6I MOUSE
9	415	61.6	107	1	KV6H MOUSE
10	415	61.6	235	2	Q7TMK0 mus musculu
11	414	61.4	107	1	KV6G MOUSE
12	411	61.0	111	2	AAR10981 mus muscu
13	411	61.0	111	2	AAR10982 mus muscu
14	411	61.0	111	2	AAR10994 mus muscu
15	410	60.8	108	2	AAR11048 mus muscu
16	409	60.7	110	2	AAR10999 mus muscu

17	408	60.5	107	1	KV6J MOUSE	P04944 mus musculu
18	398	59.1	107	2	AAR11015	Aar11015 mus muscu
19	392	58.2	106	2	Q9U410	Q9u410 schistosoma
20	386	57.3	108	1	KV6K MOUSE	P04945 mus musculu
21	385	57.1	107	1	KV6C MOUSE	P01677 mus musculu
22	380	56.4	107	1	KV6B MOUSE	P01676 mus musculu
23	379.5	56.3	214	2	Q9RIa5	Q9ria5 mus musculu
24	379	56.2	107	1	KV6A MOUSE	P01675 mus musculu
25	379	56.2	107	1	KV6D MOUSE	P01678 mus musculu
26	377	55.9	111	2	AAR11009	Aar11009 mus muscu
27	374	55.5	106	2	AAR11006	Aar11006 mus muscu
28	373.5	55.4	236	2	Q7TS98	Q7ts98 mus musculu
29	370	54.9	107	1	KV6E MOUSE	P01679 mus musculu
30	368.5	54.7	131	2	Q811C3	Q811c3 mus musculu
31	366	54.3	97	2	AAR11055	Aar11055 mus muscu
32	364	54.0	92	2	AAR11066	Aar11066 mus muscu
33	364	54.0	95	2	AAR11062	Aar11062 mus muscu
34	360.5	53.5	114	2	AAR10983	Aar10983 mus muscu
35	358.5	53.2	234	2	Q8R062	Q8r062 mus musculu
36	358	53.1	111	2	AAR11021	Aar11021 mus muscu
37	356.5	52.9	234	2	Q8VCP0	Q8vcp0 mus musculu
38	355.5	52.7	237	2	Q7SZ36	Q7sz36 xenopus lae
39	354	52.5	129	1	KV4A MOUSE	P01680 mus musculu
40	353.5	52.4	236	2	Q7Z3Y4	Q7z3y4 homo sapien
41	350.5	52.0	112	2	AAR11019	Aar11019 mus muscu
42	347.5	51.6	114	2	AAR11022	Aar11022 mus muscu
43	347.5	51.6	236	2	Q6PIH7	Q6pih7 homo sapien
44	347.5	51.6	236	2	Q6GMX9	Q6gmx9 homo sapien
45	347.5	51.6	236	2	AAH34141	Aah34141 homo sapi

ALIGNMENTS

RESULT 1
Q8K1F2 PRELIMINARY; PRT; 112 AA.
AC Q8K1F2;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516283; AAM64201.1; -.
DR PIR; H33932; H33932.
DR HSSP; Q91W12; 1AY1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 11953 MW; 4716B87FADB543ED CRC64;

Alignment Scores:
Pred. No.: 1.27e-41 Length: 112
Score: 452.00 Matches: 88
Percent Similarity: 85.71% Conservative: 8
Best Local Similarity: 78.57% Mismatches: 16
Query Match: 67.06% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x Q8K1F2 (1-112)

QY 1 GACATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCAACC 60

Db 1 AspileValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20
QY 61 ATGACCTGCAGTCCAGTTCAAGTGTAAATTACATGCACCTGGTTCACGAGGAGTCGGGC 120
Db 21 ileThrCysAsnAlaSerSerValSerTyrMetHisTrpPheGlnGlnLysProGly 40
QY 121 ACCTTCCCAAAAGAGGATTATGACACATCCAAACTGGCTTCGGAGTCCCTGCTGC 180
Db 41 ThrSerProLysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProAlaArg 60
QY 181 CTCAGTGGCAGTGGTCTGGGACAGAATTCACTGGAAATCAGTAGAGTGAAGGCTGAG 240
Db 61 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGlu 80
QY 241 GATGTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCGCTCACGTTCCGTTGG 300
Db 81 AspAlaAlaThrTyrTyrCysGlnGlnArgSerSerTyrProLeuThrPheGlyAlaGly 100
QY 301 ACCAAGCTGAGCTGAAACGGGCTGATGCTGCACCA 336
Db 101 ThrLysLeuGluLeuLysArgAlaAspAlaAlaPro 112

RESULT 2
Q91W12
ID Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
DR PDB; 1AY1; X-ray; L=23-232.
DR PDB; 1HQ4; X-ray; A/C=23-235.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.

DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Alignment Scores: 1.86e-41 Length: 235
Pred. No.: 451.00 Matches: 89
Score: Percent Similarity: 84.48% Conservative: 9
Best Local Similarity: 76.72% Mismatches: 18
Query Match: 66.91% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x Q91W12 (1-235)
QY 4 ATTGAGTCACTCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAAGGTCACCATG 63
Db 24 IlevallLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluArgValThrMet 43
QY 64 ACCTGCAGTCCAGTTCAGTGTAAATTACATGCACCTGGTTCACGAGGAGTCGGGCACC 123
Db 44 ThrCysSerAlaSerSerValSerHisMetHisTyrGlnGlnLysSerGlyThr 63
QY 124 TTCCCCAAAAGAGGATTATGACACATCCAAACTGGCTTCGGAGTCCCTGCTCGCCTC 183
Db 64 SerProLysArgTrpIleTyrAspThrPheLysLeuThrSerGlyValProAspArgPhe 83
QY 184 AGTGGCAGTGGTCTGGGACAGAAATTCACCCCTGGAAATCAGTAGACTGAAGGCTGAGGAT 243
Db 84 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerAsnMetGluAlaGluAsp 103
QY 244 GTGGGTGTGTATTACTGTCAACAACTGTAGAGTATCCGCTCACGTTCCGTTGGTGGGACC 303
Db 104 ValAlaThrTyrTyrCysGlnGlnTrpSerArgAsnProProThrPheGlyValGlyThr 123

304 AAGCTGGAGCTGAAACGGGCTGATGCTGCACCACTGTATCCATCTTC 351
124 LysLeuGluLeuLysArgAlaAspAlaAlaProThrValSerIlePhe 139

RESULT 3
Q8VDD0
ID Q8VDD0 PRELIMINARY; PRT; 134 AA.
AC Q8VDD0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-MOG Z12 variable light chain (Fragment).
GN Name=anti-MOG kappa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Sembi P.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Chernajovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ416331; CAC94866.1; -.
DR PIR; G27887; G27887.
DR HSSP; P01834; 1MIM.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.

FT NON TER 134 134
SQ SEQUENCE 134 AA; 14525 MW; CFDF8E2236E2D0CF CRC64;

Alignment Scores:

Pred. No.: 1.04e-40 Length: 134
Score: 444.00 Matches: 85
Percent Similarity: 84.68% Conservative: 9
Best Local Similarity: 76.58% Mismatches: 17
Query Match: 65.88% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x Q8VDD0 (1-134)

QY 4 ATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTACCATG 63
Db 24 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43
QY 64 ACCTGCAGTCCAGTTCAAGTGTAAATTACATGCACTGGTTCCAGCAGGAGTCGGGCACC 123
Db 44 ThrCysSerAlaSerSerIleSerTyrMetHisTrpTyrGlnGlnLysProGlyThr 63
QY 124 TTCCCCAAAGAGGATTTATGACACATCCAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db 64 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArgPhe 83
QY 184 AGTGGCAGTGGTCTGGACAGAAATTCACCTCGAAATCAGTAGAGTGAAGGTGAGGAT 243
Db 84 SerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGluAsp 103
QY 244 GTGGGTGTATTACTGTCAACAACTTGTAGAGTATCCGCTCACGTTTCGGTCTGGGACC 303
Db 104 AlaAlaThrTyrTyrCysHisGlnArgSerSerTyrProTrpThrPheGlyGlyThr 123
QY 304 AAGCTGGAGCTGAAACGGCTGATGCTGCACCA 336
Db 124 LysLeuGluIleLysArgAlaAspAlaPro 134

RESULT 4

Q8K1F0 PRELIMINARY; PRT; 112 AA.
AC Q8K1F0;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516285; AAM64203.1; -.
DR PIR; A33933; A33933.
DR PIR; PC4405; PC4405.
DR HSSP; P01837; 1ORQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1 112
FT NON TER 112 112
SQ SEQUENCE 112 AA; 11901 MW; F6644663201AA239 CRC64;

Alignment Scores:

Pred. No.: 1.73e-39 Length: 112
Score: 433.00 Matches: 84
Percent Similarity: 83.49% Conservative: 7
Best Local Similarity: 77.06% Mismatches: 18
Query Match: 64.24% Indels: 0

DB: 2 Gaps: 0
US-10-049-868A-1 (1-359) x Q8K1F0 (1-112)
QY 10 CTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTACCATGACCTGC 69
Db 4 LeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMetThrCys 23
QY 70 AGTGCCAGTTCAAGTGTAAATTACATGCACTGGTTCCAGCAGGAGTCGGGCACCTTCCCC 129
Db 24 SerAlaSerSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGlyThrSerPro 43
QY 130 AAAAGAAGGATTTATGACACATCCAACTGGCTTCTGGAGTCCCTGCTCGCTCAGTGGC 189
Db 44 LysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArgPheSerGly 63
QY 190 AGTGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGGT 249
Db 64 SerGlySerGlyAsnSerTyrSerLeuThrIleSerSerThrGluGlyGluAspAlaAla 83
QY 250 GTGTATTACTGTCAACAACTTGTAGAGTATCCGCTCACGTTTCGGTCTGGGACCAAGCTG 309
Db 84 ThrTyrTyrCysGlnGlnTrpSerSerAsnProProThrPheGlyGlyThrLysLeu 103
QY 310 GAGCTGAAACGGGCTGATGCTGCACCA 336
Db 104 GluIleLysArgAlaAspAlaPro 112

RESULT 5

KV6F_MOUSE
ID KV6F_MOUSE STANDARD; PRT; 107 AA.
AC P04940;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-17.4.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone and its early diversification."
RL Nature 304:320-324(1983).
CC -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC -----
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CC -----
DR EMBL; K00735; AAA38680.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hydridoma; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 33 Complementarity-determining-1.
FT DOMAIN 34 48 Framework-2.
FT DOMAIN 49 55 Complementarity-determining-2.
FT DOMAIN 56 87 Framework-3.
FT DOMAIN 88 96 Complementarity-determining-3.
FT DOMAIN 97 106 Framework-4.
FT DISULFID 23 87 By similarity.

FT NON TER 107 107
SQ SEQUENCE 107 AA; 11561 MW; 6F694284ECFA68E6 CRC64;

Alignment Scores:

Pred. No.: 3.83e-38 Length: 107
Score: 421.00 Matches: 82
Percent Similarity: 85.85% Conservative: 9
Best Local Similarity: 77.36% Mismatches: 15
Query Match: 62.46% Indels: 0
DB: 1 Gaps: 0

US-10-049-868A-1 (1-359) x KV6F_MOUSE (1-107)

QY 4 ATTGAGCTCAGCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATG 63
Db 2 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGlnLysValThrMet 21
QY 64 ACCTGCAGTGCAGTTCAGGTGTTAATTACATGCACCTGGTTCACGACGAGGAGTCGGGCACC 123
Db 22 ThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGlyThr 41
QY 124 TTCCCCAAAAGAAGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db 42 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArgPhe 61
QY 184 AGTGGCAGTGGTCTCTGGACAGAAATTCACCTGGAAATCAGTAGAGTCAAGGCTGAGGAT 243
Db 62 SerGlySerGlySerAlaThrSerTyrSerLeuThrIleThrSerMetGlnAlaGluAsp 81
QY 244 GTGGGTGTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTCCGGTCTGGGACC 303
Db 82 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGlyThr 101
QY 304 AAGCTGGAGCTGAAACGG 321
Db 102 LysLeuGluLeuLysArg 107

RESULT 6

Q8K1F3 PRELIMINARY; PRT; 112 AA.
AC Q8K1F3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516282; AAM64200.1; -.
DR PIR; A33933;
DR PIR; PH1085;
DR HSSP; P01837; 25C8.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;

Alignment Scores:

Pred. No.: 6.48e-38 Length: 112
Score: 419.00 Matches: 81
Percent Similarity: 83.04% Conservative: 12
Best Local Similarity: 72.32% Mismatches: 19
Query Match: 62.17% Indels: 0

DB:

US-10-049-868A-1 (1-359) x Q8K1F3 (1-112)

QY 1 GACATTGAGCTCAGCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACC 60
Db 1 AspIleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20
QY 61 ATGACCTGCAGTCCAGTTCAGGTGTTAATTACATGCACCTGGTTCACGACGAGGAGTCGGGC 120
Db 21 IleSerCysSerAlaSerSerValSerTyrMetTyrTrpTyrGlnGlnLysProGly 40
QY 121 ACCTTCCCCAAAAGAAGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 41 SerSerProLysProTrpIleTyrArgThrSerAsnLeuAlaSerGlyValProAlaArg 60
QY 181 CTCAGTGGCAGTGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTGAG 240
Db 61 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80
QY 241 GATGTGGGTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTCCGGTCTGGG 300
Db 81 AspAlaAlaThrTyrTyrCysGlnGlnTyrHisSerTyrProTyrThrPheGlyGlyGly 100
QY 301 ACCAAGCTGGAGCTGAAACGGGCTGATGCTGCACCA 336
Db 101 ThrLysLeuGluIleLysArgAlaAspAlaAlaPro 112

RESULT 7

Q8K1F1 PRELIMINARY; PRT; 114 AA.
AC Q8K1F1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516284; AAM64202.1; -.
DR PIR; A33933; A33933.
DR PIR; PH1058;
DR HSSP; P01837; 25C8.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12162 MW; 8BD9833DBF3EEFD1 CRC64;

Alignment Scores:

Pred. No.: 6.5e-38 Length: 114
Score: 419.00 Matches: 83
Percent Similarity: 80.70% Conservative: 9
Best Local Similarity: 72.81% Mismatches: 20
Query Match: 62.17% Indels: 2
DB: 2 Gaps: 1

US-10-049-868A-1 (1-359) x Q8K1F1 (1-114)

QY 1 GACATTGAGCTCAGCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACC 60
Db 1 AspIleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20
QY 61 ATGACCTGCAGTGCAGTTCAGGTGTTAATTACATGCACCTGGTTCACGACGAGGAG 114

```
Db      21 MetThrCysArgAlaSerSerValSerSerTyrLeuHisTrpTyrGlnGlnLys 40
      115 TCGGGCACCTTCCCAAAAGAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCT 174
      41 SerGlyAlaSerProLysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValPro 60
      175 GCTCGCCTCAGTGGCAGTGGGTCTGGGACAGAATTACCCCTGGAAATCAGTGAAG 234
      61 AlaArgPheSerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGlu 80
      235 GCTGAGGATGTGGGTGTGTATTACTGTCAACAACCTGTAGAGTATCCGCTCACGTTCCGGT 294
      81 AlaGluAspAlaAlaThrTyrTyrCysGlnGlnTyrHisSerTyrProArgThrPheGly 100
      295 GCTGGGACCAAGCTGGAGCTGAAACGGGCTGATCGTCACCA 336
      101 GlyGlyThrLysLeuGluIleLysArgAlaAspAlaPro 114
```

```
RESULT 8
KV6I_MOUSE
ID KV6I_MOUSE STANDARD; PRT; 107 AA.
AC P04943;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ6-8.3.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
phenyloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
```

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CC
CC EMBL; K00740; AAA38685.1; -.
CC HSSP; P01679; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 33 Complementarity-determining-1.
FT DOMAIN 34 48 Framework-2.
FT DOMAIN 49 55 Complementarity-determining-2.
FT DOMAIN 56 87 Framework-3.
FT DOMAIN 88 96 Complementarity-determining-3.
FT DOMAIN 97 106 Framework-4.
FT DISULFID 23 87 By similarity.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11572 MW; 6F694824ECF0C8E6 CRC64;
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Alignment Scores:
Pred. No.: 1.4e-37 Length: 107
Score: 416.00 Matches: 81
Percent Similarity: 84.91% Conservative: 9
Best Local Similarity: 76.42% Mismatches: 16
Query Match: 61.72% Indels: 0
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DB:
US-10-049-868A-1 (1-359) x KV6I_MOUSE (1-107)
QY      4 ATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCAACCATG 63
      2 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGlnLysValThrMet 21
      64 ACCTGCAGTGCAGTTCAAAGTGTATTATACATGCACCTGGTTCAGCAGCAGAGTCGGGCACC 123
      22 ThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGlyThr 41
      124 TTCCCCAAAGAAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTCGCCTC 183
      42 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGly**ProAlaArgPhe 61
      184 AGTGGCAGTGGGTCTGGGACAGAATTACCCCTGGAAATCAGTAGAGTGAAGGCTGAGGAT 243
      62 SerGlySerGlySerAlaThrSerTyrSerLeuThrIleThrSerMetGlnAlaGluAsp 81
      244 GTGGGTGTGTATTACTGTCAACAACCTGTAGAGTATCCGCTCACGTTCCGTTGGGACC 303
      82 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGlyThr 101
      304 AAGCTGGAGCTGAAACGG 321
      102 LysLeuGluLeulysArg 107
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```
RESULT 9
KV6H_MOUSE
ID KV6H_MOUSE STANDARD; PRT; 107 AA.
AC P04942;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ5-61.1.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
phenyloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
```

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CC
CC EMBL; K00739; AAA38684.1; -.
CC HSSP; P01679; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 33 Complementarity-determining-1.
FT DOMAIN 34 48 Framework-2.
FT DOMAIN 49 55 Complementarity-determining-2.
FT DOMAIN 56 87 Framework-3.
FT DOMAIN 88 96 Complementarity-determining-3.
FT DOMAIN 97 106 Framework-4.
FT DISULFID 23 87 By similarity.
```


RT phenyloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
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CC -----
DR EMBL; K00737; AAA38682.1; -.
DR HSSP; Q91W12; 1AY1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 33 Complementarity-determining-1.
FT DOMAIN 34 48 Framework-2.
FT DOMAIN 49 55 Complementarity-determining-2.
FT DOMAIN 56 87 Framework-3.
FT DOMAIN 88 96 Complementarity-determining-3.
FT DOMAIN 97 106 Framework-4.
FT DISULFID 23 87 By similarity.
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11556 MW; 72488DA9EF354934 CRC64;

Alignment Scores:
Pred. No.: 2.34e-37 Length: 107
Score: 414.00 Matches: 81
Percent Similarity: 84.91% Conservative: 9
Best Local Similarity: 76.42% Mismatches: 16
Query Match: 61.42% Indels: 0
DB: 1 Gaps: 0
US-10-049-868A-1 (1-359) x KV6G_MOUSE (1-107)

QY 4 ATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCCACCATG 63
Db 2 IleLeuLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGlnLysValThrMet 21
QY 64 ACCTGCAGTGCAGTTCAGTGTAAATTACATGCACATCCAACTGGCTTCTGGAGTCCGCTCGCCTC 123
Db 22 ThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGlyThr 41
QY 124 TTCCCAAAAGAGGATTATGACACATCCAACTGGCTTCTGGAGTCCGCTCGCCTC 183
Db 42 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArgPhe 61
QY 184 AGTGGCAGTGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTGAGGAT 243
Db 62 SerGlySerGlySerAlaThrSerTyrSerLeuThrIleThrSerMetGlnAlaGluAsp 81
QY 244 GTGGGTGTGTATTACTGTCAACAACTTGATAGATATCCGCTCACGTTCCGTTGGTGGGACC 303
Db 82 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGlyThr 101
QY 304 AAGCTGGAGCTGAAACGG 321
Db 102 LysLeu**LeuLysArg 107

RESULT 12
AAR10981
ID AAR10981 PRELIMINARY; PRT; 111 AA.
AC AAR10981;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice."
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436821; AAR10981.1; -.
FT NON_TER 1 1
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11819 MW; EE2F666368BC91BC CRC64;

Alignment Scores:
Pred. No.: 5.12e-37 Length: 111
Score: 411.00 Matches: 79
Percent Similarity: 81.82% Conservative: 11
Best Local Similarity: 71.82% Mismatches: 20
Query Match: 60.98% Indels: 0
DB: 2 Gaps: 0
US-10-049-868A-1 (1-359) x AAR10981 (1-111)

QY 10 CTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCCACATGACCTGC 69
Db 2 MetThrGlnThrProThrIleLeuSerAlaSerProGlyGluLysValThrMetThrCys 21
QY 70 AGTGCCAGTTCAGTGTAAATTACATGCACATCGTTCAGCAGGAGTCCGGGACCTTCCCC 129
Db 22 ArgAlaSerSerSerValSerTyrMetHisTrpTyrGlnGlnLysProGlySerSerPro 41
QY 130 AAAAGAAGGATTATGACACATCCAACTGGCTTCTGGAGTCCCTGCTCGCTCAGTGGC 189
Db 42 LysProTrpIleTyrAlaThrSerAsnLeuAlaSerGlyValProAlaArgPheSerGly 61
QY 190 AGTGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGT 249
Db 62 SerGlySerGlyThrSerTyrSerLeuThrIleSerArgValGluAlaGluAspAlaAla 81
QY 250 GTGTATTACTGTCAACAACTTGATAGATATCCGCTCACGTTCCGTTGGTGGGACCAAGCTG 309
Db 82 ThrTyrTyrCysGlnGlnTrpSerSerAsnProProThrPheGlyGlyThrLysLeu 101
QY 310 GAGCTGAAACGGCTGATGCTGCACCACT 339
Db 102 GluIleLysArgAlaAspAlaAlaProThr 111

RESULT 13
AAR10982
ID AAR10982 PRELIMINARY; PRT; 111 AA.
AC AAR10982;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice."
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436822; AAR10982.1; -.
FT NON_TER 1 1
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11819 MW; EE2F666368BC91BC CRC64;

Alignment Scores:

```
Pred. No.: 5.12e-37 Length: 111
Score: 411.00 Matches: 79
Percent Similarity: 81.82% Conservative: 11
Best Local Similarity: 71.82% Mismatches: 20
Query Match: 60.98% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x AAR10982 (1-111)

QY 10 CTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCACCATGACCTGC 69
Db 2 MetThrGlnThrProThrIleLeuSerAlaSerProGlyGluLysValThrMetThrCys 21

QY 70 AGTGCCAGTCAAGTGTTAATTACATGCACTGGTTCAGCAGGAGTCGGGCACCTTCCCC 129
Db 22 ArgAlaSerSerSerValSerTyrMetHisTrpTyrGlnGlnLysProGlySerSerPro 41

QY 130 AAAAGAAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTCAGTGGC 189
Db 42 LysProTrpIleTyrAlaThrSerAsnLeuAlaSerGlyValProAlaAArgPheSerGly 61

QY 190 AGTGGTCTGGACAGAAATTCACCTTGGAATCAGTAGAGTGAAGGCTGAGGATGTGGGT 249
Db 62 SerGlySerGlyThrSerTyrSerLeuThrIleSerArgValGluAlaGluAspAlaAla 81

QY 250 GTGTATTACTGTCAACAACCTTGTAGATATCCGCTCACGTTCCGTTGGTGGGACCAAGCTG 309
Db 82 ThrTyrTyrCysGlnGlnTrpSerSerAsnProProThrPheGlyGlyThrLysLeu 101

QY 310 GAGCTGAAACGGGCTGATGCTGCACCAACT 339
Db 102 GluIleLysArgAlaAspAlaAProThr 111

RESULT 14
AAR10994
ID AAR10994 PRELIMINARY; PRT; 111 AA.
AC AAR10994;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436834; AAR10994.1; -.
FT NON_TER 1 111
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11914 MW; 69E94859D33DA6BF CRC64;

Alignment Scores:
Pred. No.: 5.12e-37 Length: 111
Score: 411.00 Matches: 77
Percent Similarity: 83.64% Conservative: 15
Best Local Similarity: 70.00% Mismatches: 18
Query Match: 60.98% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x AAR10994 (1-111)

QY 10 CTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCACCATGACCTGC 69
Db 2 MetThrGlnThrProAlaIleMetSerAlaSerSerGlyGluLysValThrMetThrCys 21

QY 70 AGTGCCAGTCAAGTGTTAATTACATGCACTGGTTCAGCAGGAGTCGGGCACCTTCCCC 129
Db 22 SerAlaSerSerSerIleSerTyrLeuTyrTrpTyrGlnGlnLysProGlySerSerPro 41
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QY 130 AAAAGAAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTCAGTGGC 189
Db 42 ArgLeuLeuIleTyrAspThrSerAsnLeuAlaSerGlyValProIleArgPheThrGly 61

QY 190 AGTGGTCTGGGACAGAAATTCACCTTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGGT 249
Db 62 SerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGluAspAlaAla 81

QY 250 GTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTCCGTTGGTGGGACCAAGCTG 309
Db 82 ThrTyrTyrCysGlnGlnTrpSerSerTyrProLeuThrValGlyThrGlyThrLysLeu 101

QY 310 GAGCTGAAACGGGCTGATGCTGCACCAACT 339
Db 102 GluLeuLysArgAlaAspAlaAProThr 111

RESULT 15
AAR11048
ID AAR11048 PRELIMINARY; PRT; 108 AA.
AC AAR11048;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436888; AAR11048.1; -.
FT NON_TER 1 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11738 MW; C11222F2FD9BFC160 CRC64;

Alignment Scores:
Pred. No.: 6.61e-37 Length: 108
Score: 410.00 Matches: 77
Percent Similarity: 84.11% Conservative: 13
Best Local Similarity: 71.96% Mismatches: 17
Query Match: 60.83% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x AAR11048 (1-108)

QY 10 CTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCACCATGACCTGC 69
Db 1 MetThrGlnThrProAlaIleMetSerAlaSerProGlyGluLysValThrMetThrCys 20

QY 70 AGTGCCAGTCAAGTGTTAATTACATGCACTGGTTCAGCAGGAGTCGGGCACCTTCCCC 129
Db 21 SerAlaSerSerSerValSerTyrMetTyrTrpTyrGlnGlnLysProGlySerSerPro 40

QY 130 AAAAGAAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTCAGTGGC 189
Db 41 ArgLeuLeuIleTyrAspThrSerAsnLeuAlaSerGlyValProValArgPheSerGly 60

QY 190 AGTGGTCTGGGACAGAAATTCACCTTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGGT 249
Db 61 SerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGluAspAlaAla 80

QY 250 GTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTCCGTTGGTGGGACCAAGCTG 309
Db 81 ThrTyrTyrCysGlnGlnTrpSerSerTyrProTrpThrPheGlyGlyThrLysLeu 100

QY 310 GAGCTGAAACGGGCTGATGCT 330
Db 101 GluIleLysArgAlaAspAla 107
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Search completed: October 13, 2004, 13:28:05
Job time : 104.175 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 13, 2004, 13:00:14 ; Search time 82.0429 Seconds
(without alignments)
3139.425 Million cell updates/sec

Title: US-10-049-868A-1
Perfect score: 674
Sequence: 1 gacattgagctcaccagtc.....gtatccatcttcaagcttcc 359

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 4004546

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USFTO_spool_p/US10049868/runat_13102004_132816_24785/app_query.fasta_1.1038
-DB=A Geneseq_23Sep04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10049868 @CGN_1_1_308 @runat_13102004_132816_24785 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_23Sep04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			Match	Length	DB ID	Description
	Score	Match	Length				
1	471	69.9	215	7	ADE06764		Ade06764 D18 light
2	466	69.1	144	8	ADM79827		Adm79827 Mouse IgG
3	460	68.2	135	2	AAR08347		Aar08347 Light cha
4	459	68.1	129	5	ABB75616		Abb75616 Anti-RANK
5	458	68.0	235	2	AAW41392		Aaw41392 Chimeric
6	452	67.1	108	2	AAR21301		Aar21301 Murine VL
7	452	67.1	156	8	ADO43520		Ado43520 Amino aci
8	451	66.9	215	2	AAR43674		Aar43674 Mouse ant
9	451	66.9	215	2	AAR99644		Aar99644 Anti-bGH
10	451	66.9	215	2	AAR97377		Aar97377 Murine an

11	448	66.5	108	2	AAR21293		Aar21293 Murine VL
12	445	66.0	235	2	AAR13060		Aar13060 Monoclona
13	444	65.9	241	6	ABR62010		AbR62010 Single-ch
14	444	65.9	255	3	ABR11398		AbR11398 E. coli e
15	444	65.9	255	4	AAB74199		Aab74199 PelB-scFv
16	444	65.9	255	4	AAB70769		Aab70769 Expressio
17	444	65.9	255	4	AAW72020		Aaw72020 E. caroto
18	443.5	65.8	214	2	AAW15933		Aaw15933 Antibody
19	443	65.7	118	6	AAE37758		Aae37758 Murine TI
20	443	65.7	118	6	AAE37807		Aae37807 Murine TI
21	441	65.4	316	2	AAW32086		Aay32086 Single ch
22	439	65.1	108	2	AAR21303		Aar21303 Murine VL
23	439	65.1	108	2	AAW41388		Aaw41388 Anti-CEA
24	439	65.1	266	8	ADH77307		Adh77307 Yeast kil
25	439	65.1	309	4	AAB70841		Aab70841 SNV-env 1
26	437	64.8	236	2	AAW34096		Aay34096 Partial a
27	437	64.8	241	2	ABB76197		Abb76197 Anti-meso
28	437	64.8	241	4	AAW50019		Aab50019 Antimesot
29	437	64.8	288	2	AAW82482		Aaw82482 Mouse bis
30	437	64.8	539	3	AAW50823		Aay50823 Fv-antibo
31	437	64.8	554	3	AAW50822		Aay50822 Fv-antibo
32	437	64.8	562	6	ABR57059		Abr57059 Plasmid p
33	436	64.7	109	6	ABU63531		Abu63531 Anti-cucu
34	435	64.5	108	2	AAR21294		Aar21294 Murine VL
35	435	64.5	108	2	AAR21292		Aar21292 Murine VL
36	435	64.5	330	4	AAB70842		Aab70842 SNV-env 1
37	434.5	64.5	208	2	AAW44175		Aay44175 MAb FabI3
38	433	64.2	108	2	AAR79884		Aar79884 Anti-EGFR
39	433	64.2	108	3	AAW12461		Aab12461 IgG monoc
40	433	64.2	241	5	AAW48925		Aam48925 scFv anti
41	432	64.1	108	3	AAW97236		Aay97236 Variable
42	432	64.1	108	4	AAW82710		Aab82710 VEGF anta
43	432	64.1	108	5	AAE25956		Aae25956 Mouse ant
44	432	64.1	108	5	AAU74413		Aau74413 Antigen-b
45	432	64.1	108	6	ABJ26725		Abj26725 VEGF bind

ALIGNMENTS

RESULT 1

ADE06764

ID ADE06764 standard; protein; 215 AA.

XX

AC ADE06764;

XX

DT 29-JAN-2004 (first entry)

XX

DE D18 light chain protein SEQ ID NO:34.

XX

hybrid polypeptide; protein aggregation; prion polypeptide;
neuroprotective; nootropic; antidiabetic; anticonvulsant;
cerebroprotective; antiparkinsonian; cytostatic; nephrotropic; cardiant;
antiinflammatory; antiarteriosclerotic; gene therapy;
Creutzfeldt-Jakob disease; scrapie and bovine spongiform encephalopathy;
Alzheimer's disease; Type II diabetes; Huntington's disease;
immunoglobulin amyloidosis; amyloidosis; chronic inflammatory disease;
Kw amyotrophic lateral sclerosis; Pick's disease; Parkinson's disease;
Kw Frontotemporal dementia; multiple myeloma; plasma cell dyscrasia;
Kw familial amyloidotic polyneuropathy; medullary carcinoma;
Kw chronic renal failure; congestive heart failure; chronic inflammation;
Kw atherosclerosis.

XX Synthetic.

OS

XX WO2003085086-A2.

PN

XX 16-OCT-2003.

PD

XX 08-APR-2003; 2003WO-US010856.

PF

XX 09-APR-2002; 2002US-0371610P.

PR

XX (SCRI) SCRIPPS RES INST.

PA

CC products of antibody, comprising the produced antibodies or 2D7 antibody;
CC (6) antitumour agents containing the degradation products of antibody,
CC comprising the produced antibodies or 2D7 antibody; and (7) remedies for
CC autoimmune diseases containing the degradation products of antibody,
CC comprising the produced antibodies or 2D7 antibody. The 2D7 antibody has
CC cytotstatic, immunosuppressive, antiinflammatory and dermatological
CC activities. The cell death-inducing agents are applicable in antitumour
CC agents and remedies for autoimmune diseases for treating e.g. cancer,
CC Crohn's disease and systemic lupus erythematosus. The present sequence
CC represents a mouse IgG2b light chain, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 144 AA;

Alignment Scores:
Pred. No.: 1.32e-40 Length: 144
Score: 466.00 Matches: 90
Percent Similarity: 85.34% Conservative: 9
Best Local Similarity: 77.59% Mismatches: 17
Query Match: 59.14% Indels: 0
DB: 8 Gaps: 0

US-10-049-868A-1 (1-359) x ADM79827 (1-144)

QY 4 ATTGAGCTCACCAGTCTCCAGCAATCATGTGTCATCTCCAGGGGAGAAGTCCACCATG 63
Db 24 IlevallLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrIle 43
QY 64 ACCTGCAGTGCAGTTCAGTGTTAATTACATGCACCTGGTTCCAGCAGGAGTCGGGCACC 123
Db 44 ThrCysSerAlaSerSerValSerTyrMetHisTrpPheGlnGlnLysProGlyThr 63
QY 124 TTCCCCAAAAGAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db 64 PheProLysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProThrArgPhe 83
QY 184 AGTGGCAGTGGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTGAGGAT 243
Db 84 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGluAsp 103
QY 244 GTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCGCTCACGTTCCGTCTGGGACC 303
Db 104 AlaAlaThrTyrTyrCysGlnGlnArgThrSerTyrProProThrPheGlySerGlyThr 123
QY 304 AAGCTGGAGCTGAAACGGGTGATGCTGCGACCAACTGTATCCATCTTC 351
Db 124 LysLeuGluIleLysArgAlaAspAlaAlaProThrValSerIlePhe 139

RESULT 3
AAR08347

ID AAR08347 standard; protein; 135 AA.

XX AAR08347;

DT 25-MAR-2003 (revised)

DT 05-MAR-1991 (first entry)

XX Light chain variable region of the BMA-031 Mab.

XX Human alpha/beta T-cell receptor; TCR; cancer; autoimmune disease.

OS Homo sapiens.

Key Location/Qualifiers
FH Peptide 1. .22 /label= Signal peptide
FT /label= 46. .55 CDR 1
FT Active-site 71. .77 /label= CDR 2
FT Active-site 110. .118 /label= CDR 3
FT
XX

PN EP403156-A.
XX 19-DEC-1990.
XX 07-JUN-1990; 90EP-00306178.
XX 07-JUN-1989; 89US-00362549.
PR 25-MAY-1990; 90US-00529979.
XX (GENZ) GENZYME CORP.
PA (BEHW) BEHRINGWERKE AG.
XX
PI Kurrie R, Shearman CW, Moore GP, Seiler F;
XX
DR WPI; 1990-377880/51.
DR N-PSDB; AAQ06956, AAQ06958.
XX
PT Anti-human alpha-beta T-cell receptor monoclonal antibodies - used for
PT immunosuppressive therapy in transplantation and as therapeutic agent for
PT immuno-regulation, e.g. to treat cancer.
XX
PS Disclosure; Table 1B; 44pp; English.
XX
CC The Mab recognises the epitope on alpha/beta TCR and includes a mediator
CC response. It is highly effective in clinical application before, after and
CC during bone marrow transplant surgery, in treatment of cancer and
CC autoimmune diseases, and has applications in immunoregulation. Abs may
CC also be used in detection of immunocompetent T-cells. (Updated on 25-MAR-
CC 2003 to correct PA field.)
XX
SQ Sequence 135 AA;

Alignment Scores:
Pred. No.: 5.64e-40 Length: 135
Score: 460.00 Matches: 90
Percent Similarity: 87.50% Conservative: 8
Best Local Similarity: 80.36% Mismatches: 14
Query Match: 68.25% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x AAR08347 (1-135)

QY 4 ATTGAGCTCACCAGTCTCCAGCAATCATGTGTCATCTCCAGGGGAGAAGTCCACCATG 63
Db 24 IlevallLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43
QY 64 ACCTGCAGTGCAGTTCAGTGTTAATTACATGCACCTGGTTCCAGCAGGAGTCGGGCACC 123
Db 44 ThrCysSerAlaThrSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGlyThr 63
QY 124 TTCCCCAAAAGAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db 64 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArgPhe 83
QY 184 AGTGGCAGTGGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTGAGGAT 243
Db 84 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGluAsp 103
QY 244 GTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCGCTCACGTTCCGTCTGGGACC 303
Db 104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGlyThr 123
QY 304 AAGCTGGAGCTGAAACGGGTGATGCTGCACCAACTGCTGCACCAACT 339
Db 124 LysLeuGluLeuLysArgAlaAspAlaAlaProThr 135

RESULT 4
ABB75616
ID ABB75616 standard; protein; 129 AA.
XX
AC ABB75616;
XX
DT 10-JUN-2002 (first entry)

XX Anti-RANK ligand mAb 19H22 light chain variable region.

DE RANK ligand; RANK-L; monoclonal antibody; mAb; 19H22; antibody;

XX complementarity determining region; CDR; rheumatoid arthritis;

KW osteoporosis; bone cancer; metastasis; osteolysis; osteoarthritis;

KW psoriasis; inflammatory bowel disease; multiple sclerosis; diabetes;

KW cytostatic; antiarthritic; antiinflammatory; osteopathic; antidiabetic;

KW antirheumatic; immunosuppressive; antipsoriatic; neuroprotective;

XX light chain; VL; mouse.

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT Region 24..33

FT /label= CDR1

FT /note= "complementarity determining region 1"

FT Region 49..55

FT /label= CDR2

FT /note= "complementarity determining region 2"

FT Region 88..96

FT /label= CDR3

FT /note= "complementarity determining region 3"

XX

PN WO200215846-A2.

XX

PD 28-FEB-2002.

XX

PF 21-AUG-2001; 2001WO-US026161.

XX

PR 21-AUG-2000; 2000US-0226524P.

PR 07-SEP-2000; 2000US-0230639P.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Sweet RW, Tornetta MA, Truneh A, Wattam TA;

XX

DR WPI; 2002-242022/29.

DR N-PSDB; ABL53530.

XX

PT A mouse monoclonal antibody 19H22 for treating or preventing osteopenic

PT disease including rheumatoid arthritis and osteoporosis.

XX

PS Claim 6; Page 7; 45pp; English.

XX

CC The present sequence is that of the light chain variable region of

CC claimed anti-human RANK ligand (RANK-L) murine monoclonal antibody (mAb)

CC 19H22 (isotype IgG2b/kappa). The mAb is produced by hybridoma cells

CC obtained by immunising CB6 f1 mice with human RANK-L protein, and fusing

CC spleen cells with X63-Ag8.653 myeloma cells. 19H22 mAb is specific for

CC human RANK-L, having a binding affinity characterised by a dissociation

CC constant of about 10 power -10 M. RANK-L is a member of the tumour

CC necrosis factor family of proteins and a key regulator of the immune

CC system, bone development and homeostasis. The invention provides altered,

CC chimeric and humanised 19H22 antibodies, including Fab or F(ab')2

CC fragments, antibodies comprising the light and heavy chain variable

CC regions of 19H22, and antibodies comprising the complementarity

CC determining regions of 19H22. These are used in methods for the

CC diagnosis, treatment and prevention of osteopenic diseases, including

CC rheumatoid arthritis, osteoporosis, metastatic and primary bone cancer,

CC wear debris induced osteolysis or osteoarthritis, and immune diseases

CC including psoriasis, insulin dependent diabetes, inflammatory bowel

CC disease or multiple sclerosis. Methods are also provided for the

CC recombinant production of the antibodies, using isolated nucleic acids

CC and transfected host (preferably mammalian) host cells, and a method of

CC diagnosing conditions associated with Th1 T-cell activity or osteoclast

CC development and activation, in particular those listed above

XX

SQ Sequence 129 AA;

Alignment Scores: 7.15e-40 Length: 129

Pred. No.: 7.15e-40 Length: 129

Score: 459.00 Matches: 89

Percent Similarity: 86.21% Conservative: 11

Best Local Similarity: 76.72% Mismatches: 16

Query Match: 68.10% Indels: 0

DB: 5 Gaps: 0

US-10-049-868A-1 (1-359) x ABB75616 (1-129)

QY 4 ATTGAGTCACTCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGAGAGGTCAACCAATG 63

Db 2 I l e v a l l e u T h r G l n S e r P r o A l a l l e M e t S e r A l a S e r P r o G l y G l u L y s V a l T h r M e t 21

QY 64 ACCTGCAGTCCAGTTCAACTGTTAATTACATGCACCTGGTTCACGAGGAGTCGGGCACC 123

Db 22 T h r C y s S e r A l a S e r S e r V a l S e r T y r M e t T y r T r p T y r G l n G l n L y s P r o G l y S e r 41

QY 124 TTCCCAAAAGAGGATTTATGACATCCAAACTGGCTTCGGAGTCCCTGCTCGCCTC 183

Db 42 S e r P r o A r g L e u L e u I l e T y r A s p T h r S e r A s n L e u A l a S e r G l y V a l P r o V a l A r g P h e 61

QY 184 AGTGGCAGTGGGTCTGGGACAGAAATTCACCTCGAAATCAGTAGAGTGAAGGCTGAGGAT 243

Db 62 S e r G l y S e r G l y S e r G l y T h r S e r T y r S e r L e u T h r I l e S e r A r g M e t G l u A l a G l u A s p 81

QY 244 GTGGGTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTACGTTCCGTTGCTGGGACC 303

Db 82 A l a A l a T h r T y r T y r C y s G l n G l n T r p S e r A s n P h e P r o L e u T h r P h e G l y A l a G l y T h r 101

QY 304 AAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351

Db 102 L y s L e u G l u L e u L y s A r g A l a A s p A l a A l a P r o T h r V a l S e r I l e P h e 117

RESULT 5

AAW41392

ID AAW41392 standard; protein; 235 AA.

XX

AC AAW41392;

XX

DT 17-OCT-2003 (revised)

DT 02-JUN-1998 (first entry)

XX

DE Chimeric anti-CEA antibody 806.077 light chain.

XX

KW Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;

KW cancer diagnosis; complementarity determining region; light chain.

XX

OS Homo sapiens.

OS Mus sp.

OS Chimeric.

XX

PN WO9742329-A1.

XX

PD 13-NOV-1997.

XX

PF 29-APR-1997; 97WO-GB001165.

XX

PR 04-MAY-1996; 96GB-00009405.

PR 14-FEB-1997; 97GB-00003103.

XX

PA (ZENE) ZENECA LTD.

XX

PI Copley CG, Edge MD, Emery SC;

XX

DR WPI; 1997-558987/51.

DR N-PSDB; AAV17288.

XX

PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for diagnosis

PT and therapy of cancer.

XX

PS Example 8; Page 100-101; 208pp; English.

XX

CC This sequence is the light chain variable region of the antibody of the

CC invention. The antibody is an anti-CEA (carcinoembryonic antigen)

CC antibody (806.077 Ab).. Host cells or transgenic organisms transformed
CC with DNA encoding the antibody, are used to make the antibody or
CC conjugate. The conjugate is used in a medicament suitable for intravenous
CC administration. The conjugate can be used for cancer therapy, selectively
CC killing tumour cells. The antibody can be used for in vivo or in vitro
CC diagnosis of cancer. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 235 AA;

Alignment Scores:
Pred. No.: 1.01e-39 Length: 235
Score: 458.00 Matches: 90
Percent Similarity: 83.76% Conservative: 8
Best Local Similarity: 76.92% Mismatches: 19
Query Match: 67.95% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x AAW41392 (1-235)

QY 1 GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCACC 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
23 AsplleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 42
QY 61 ATGACCTGCAGTCCAGTTCAGTGTAAATACATGCACCTGGTTCACGAGGAGTCGGGC 120
Db :::
43 IleThrCysSerAlaSerSerValThrTyrMetHisTrpPheGlnLysProGly 62
QY 121 ACCTTCCCCAAAGAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db ||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||
63 ThrSerProLysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProAlaArg 82
QY 181 CTCAGTGGCAGTGGTCTGGGACAGAAATTCACCCCTGGAAATCAGTAGAGTGAAGGCTGAG 240
Db ||||||||||||||||||||||||||| ::::: ||| ||||||| ::::: |||
83 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGlu 102
QY 241 GATGTGGGTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTCCGGTGGG 300
Db ||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||
103 AspAlaAlaThrTyrTyrCysGlnGlnArgSerThrTyrProLeuThrPheGlyAlaGly 122
QY 301 ACCAAGCTGGAGCTGAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db ||||||||||| ::::: ||| ||||||| ::::: ||| |||||||
123 ThrLysLeuGluIleLysArgThrValAlaAlaProSerValPheIlePhe 139

RESULT 6
AAR21301
ID AAR21301 standard; protein; 108 AA.

XX AAR21301;
AC AAR21301;
DT 21-MAY-1992 (first entry)
XX
DE Murine VL kappa group IV/VI chain p specific for pOx.
XX
KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
KW g3p; binding; adsorption; gene VIII; diverse repertoire;
KW specific binding pairs; replicable genetic display package.
XX

OS Synthetic.
XX
XX
PH Key Location/Qualifiers
FT Binding-site 24. .33
FT /label= CDR1
FT Binding-site 49. .55
FT /label= CDR2
FT Binding-site 88. .96
FT /label= CDR3
FT /note= " D-X-G-X-X motif "
XX

PN WO9201047-A.
XX
XX 23-JAN-1992.
PD
XX
PF 10-JUL-1990; 90GB-00015198.

XX
PR 10-JUL-1990; 90GB-00015198.
PR 19-OCT-1990; 90GB-00022845.
PR 12-NOV-1990; 90GB-00024503.
PR 06-MAR-1991; 91GB-00004744.
PR 15-MAY-1991; 91GB-00010549.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA (MEDI-) MED RES COUNCIL.
XX
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD;
XX
DR WPI; 1992-056862/07.
XX
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic display
PT package.
XX

PS Example 22; Fig 24; 209pp; English.

XX
CC The VK sequence is one of 23 (AAR21286-308) expressed from a single chain
CC Fv library. The library produces a diverse repertoire of antibody
CC fragments specific for 2-phenyl-5-oxazolone (pOx). It was prepd. using
CC cDNA generated from mRNA from mice immunised with pOx coupled to chicked
CC serum albumin. The VH and VL kappa sequences were separately amplified by
CC PCR (AAQ23474-84) and ligated into fdCAT2 (AAQ23463) for expression on
CC the phage surface as fusions with gene III. The resulting library of
CC clones was diverse; 23 hapten binding clones were sequenced revealing 8
CC VH genes (A-H; AAR21264-71) in a variety of pairings with 7 Vk genes (a-g
CC ; AAR21286-92). Most clones were VH-B combinations so a further
CC hierarchical library was prepd. by "crossing" VH-B with the Vk
CC repertoire. The resulting library was screened for hapten binding and 24
CC clones sequenced. 14 new partners (AAR21293-308) for VH-B were
CC identified. Nearly all the Vk genes were "ox-like"; only f, (from the
CC original library) and h, p, q, and r (from the hierarchical library) were
CC Vkox1 type genes. Of the 24 hierarchical clones, 2 were of type "p". The
CC Kd of VH-B/Vk-d for pOx-GABA was 10 nM, one of the highest values found.
CC This suggests that phage bearing scFv fragments having weak affinities
CC can be selected with antigen, probably due to the avidity of the multiple
CC antibody heads on the phage. The different combinations could also be
CC isolated on a basis of antigen affinity. See also AAR21260-307, 309-311;
CC AAR22450, 565-581

XX Sequence 108 AA;

Alignment Scores:
Pred. No.: 3.84e-39 Length: 108
Score: 452.00 Matches: 88
Percent Similarity: 88.89% Conservative: 8
Best Local Similarity: 81.48% Mismatches: 12
Query Match: 67.06% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x AAR21301 (1-108)

QY 1 GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCACC 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 AsplleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20
QY 61 ATGACCTGCAGTCCAGTTCAGTGTAAATACATGCACCTGGTTCACGAGGAGTCGGGC 120
Db ||||||||||||||||||||||||||| ::::: ||| ||||||| ::::: |||
21 MetThrCysSerAlaSerSerSerValSerTyrMetHisTrpTyrGlnLysSerGly 40
QY 121 ACCTTCCCCAAAGAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db ||| |||||| |||||| |||||| |||||| |||||| |||||| |||||| |||
41 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArg 60
QY 181 CTCAGTGGCAGTGGTCTGGGACAGAAATTCACCCCTGGAAATCAGTAGAGTGAAGGCTGAG 240
Db |||||||||||||||||||||||| ::::: ||| ||||||| ::::: |||
61 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80
QY 241 GATGTGGGTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTCCGCTGGG 300

Db 81 AspValAlaThrTyrTyrCysGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 100
QY 301 ACCAAGCTGGAGCTGAAACGGGCT 324
Db 101 ThrLysLeuGluIleLysArgAla 108
RESULT 7
ADO43520
ID ADO43520 standard; protein; 156 AA.
XX
AC ADO43520;
XX
DT 29-JUL-2004 (first entry)
XX
DE Amino acid sequence of variable light chain of antibody BF11.
XX
KW antibody; lipase; biocatalysis; bioconversion; fragrance; flavour;
KW detergent; light chain; monoclonal antibody BF11.
XX
OS Mus musculus.
XX
PN WO2004039845-A1.
XX
PD 13-MAY-2004.
XX
PF 31-OCT-2002; 2002WO-EP012149.
XX
PR 31-OCT-2002; 2002WO-EP012149.
XX
PA (UYRO-) UNIV ROMA DEGLI STUDI LA SAPIENZA.
XX
PI Frati L, Biffoni M, Rughetti A, Koshkaki HR, Barachini S, Nuti M;
PI Palocci C, Soro S, Cernia E;
XX
DR WPI; 2004-376166/35.
DR N-PSDB; ADO43519.
XX
PT New antibodies and polypeptides that recognize microbial lipases and
PT enhance the hydrolytic activity of the enzyme, useful for e.g.
PT biocatalysis or bioconversion reactions, in biosensor technology or
PT bioremediation.
XX
PS Claim 11; Page 32; 42pp; English.
XX
CC The specification describes antibodies or polypeptides for microbial
CC lipase, which enhance the hydrolytic activity of the enzyme. The
CC polypeptides, antibodies or immunocomplex are useful for biocatalysis or
CC bioconversion reactions (e.g. hydrolysis, interesterification,
CC esterification, alcoholysis, acidolysis or aminolysis); in biosensor
CC technology; in bioremediation; in preparing fragrances or flavours and in
CC chemical modification of alcohols, acids, esters or fats; in cosmetic,
CC pharmaceutical and food industries; in preparing detergents; or in
CC identifying, purifying or measuring microbial lipases. The present
CC sequence represents the variable light chain of monoclonal antibody BF11,
CC which is directed against the Candida rugosa lipase.
XX
SQ Sequence 156 AA;
Alignment Scores:
Pred. No.: 4.08e-39 Length: 156
Score: 452.00 Matches: 88
Percent Similarity: 84.62% Conservative: 11
Best Local Similarity: 75.21% Mismatches: 18
Query Match: 67.06% Indels: 0
DB: 8 Gaps: 0
US-10-049-868A-1 (1-359) x ADO43520 (1-156)
QY 1 GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCACC 60
Db 1 GluLeuValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20

QY 61 ATGACCTGCAGTGCCAGTTCAAGTGTTAATTACATGCACCTGGTTCACGAGGAGTCGGGC 120
Db 21 MetThrCysSerAlaSerSerValArgTyrIleHisTrpTyrGlnGlnLysSerGly 40
QY 121 ACCTTCCCCAAAAGAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 41 ThrSerProLysArgTrpIleTyrValThrSerLysArgAlaSerGlyValProAlaArg 60
QY 181 CTCAGTGGCAGTGGGTCTGGGACAGAATTCCACCTGGAATCAGTAGAGTGAAGGCTGAG 240
Db 61 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80
QY 241 GATGTGGGTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTCCGTGCTGGG 300
Db 81 AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProPheThrPheGlySerGly 100
QY 301 ACCAAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db 101 ThrLysLeuGluIleLysArgAlaAspAlaProThrValSerIlePhe 117
RESULT 8
AAR43674
ID AAR43674 standard; protein; 215 AA.
XX
AC AAR43674;
XX
DT 25-MAR-2003 (revised)
DT 23-MAY-1994 (first entry)
XX
DE Mouse anti-bovine growth hormone Mab light chain.
XX
KW Monoclonal antibody; MAb; affinity; binding; antigen; diagnostics;
KW therapy; imaging; purification; biosensors.
XX
OS Mus musculus.
XX
PN US5260203-A.
XX
PD 09-NOV-1993.
XX
PF 25-APR-1990; 90US-00512910.
XX
PR 02-SEP-1986; 86US-00902971.
PR 02-SEP-1987; 87US-00092110.
PR 19-JAN-1989; 89US-00299617.
XX
PA (ENZO-) ENZON LABS INC.
XX
PI Ladner RC, Bird RE, Hardman K;
XX
DR WPI; 1993-367875/46.
DR N-PSDB; AAQ51535.
XX
PT Single chain poly:peptide for binding antigen - comprising light and
PT heavy chain antigen binding portions linked by peptide linker.
XX
PS Disclosure; Fig 22; 78pp; English.
XX
CC This sequence is the mature light chain of a monoclonal antibody (Mab)
CC and is the starting material for the production of a single chain
CC polypeptide having binding affinity for a given antigen (Bovine growth
CC hormone). The polypeptide comprises a first polypeptide comprising the
CC antigen binding portion of the light chain variable region of an
CC antibody and a second polypeptide comprising the antigen binding portion
CC of the heavy chain variable region of an antibody and at least one
CC peptide linker linking the first and second polypeptide chains. The
CC resulting single chain polypeptide can be used in diagnostics, therapy
CC (in vivo and in vitro), imaging, purifications and biosensors. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PA field.)
XX
SQ Sequence 215 AA;

Alignment Scores: 5.49e-39 Length: 215
Pred. No.: 451.00 Matches: 91
Score: 83.62% Conservative: 6
Percent Similarity: 78.45% Mismatches: 17
Best Local Similarity: 66.91% Indels: 2
Query Match: 2 Gaps: 1
DB: 1

US-10-049-868A-1 (1-359) x AAR43674 (1-215)

QY 10 CTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGC 69
Db 4 LeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMetThrCys 23

QY 70 AGTGCCAGTCAAGTGTT-----AATTACATGCACTGGTTCCAGCAGGAGTCGGGCACC 123
Db 24 ArgAlaSerSerValSerSerTyrLeuHisTrpPheGlnGlnLysSerGlyAla 43

QY 124 TTCCCCAAAAGAGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db 44 SerProLysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProAlaArgPhe 63

QY 184 AGTGGCAGTGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTGAGGAT 243
Db 64 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerValGluAlaGluAsp 83

QY 244 GTGGGTGTGTTACTGTCAACAACTTGAGAGTATCCGCTCACGTTCCGTTGCTGGGACC 303
Db 84 AlaAlaThrTyrTyrCysGlnGlnTyrSerGlyTyrProLeuThrPheGlyAlaGlyThr 103

QY 304 AAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db 104 LysLeuGluLeuLysArgAlaAspAlaProThrValSerIlePhe 119

RESULT 9
AAR99644
ID AAR99644 standard; protein; 215 AA.
XX AAR99644;
AC AAR99644;
XX 25-MAR-2003 (revised)
DT 11-OCT-1996 (first entry)
XX
DE Anti-bGH monoclonal antibody light chain.
XX
KW Antibody engineering; single polypeptide chain binding molecule;
KW heavy chain; light chain; monoclonal antibody; MAB;
KW bovine growth hormone; bGH; immunoaffinity purification.
XX
OS Mus sp.
XX
PN US5534621-A.
XX
PD 09-JUL-1996.
XX
PF 06-JUN-1995; 95US-00468992.
XX
PR 02-SEP-1986; 86US-00902971.
PR 02-SEP-1987; 87US-00092110.
PR 19-JAN-1989; 89US-00299617.
PR 25-APR-1990; 90US-00512910.
PR 01-APR-1993; 93US-00040440.
XX
PA (ENZO-) ENZON LABS INC.
XX
PI Bird RE, Ladner RC, Hardman K;
XX
DR WPI; 1996-333309/33.
DR N-PSDB; AAT13734.
XX
PT Immuno:purificn. using single binding chain molecule including antigen-
PT binding parts of antibody light and heavy chain variable regions
PT connected by a linker - is smaller, stabler and less expensive than

complete antibodies.
XX Example; Fig 22; 78pp; English.
XX The mature heavy chain (AAR99643) and mature light chain (AAR99644) of the mouse anti-bovine growth hormone monoclonal antibody 3C2 can be utilised in novel single chain binding molecules (AAR99645-48), in which the hypervariable regions from IGG1 3C2 MAb are joined by peptide linkers derived from the Fv regions of an IgA class anti-phosphorylcholine myeloma antibody, MCPC-603. The single chain molecules retain the binding specificity of the light and heavy chains and have the advantages of smaller size, greater stability and reduced cost. They can be used in therapy, diagnostics, imaging, purification and biosensors. (Updated on 25-MAR-2003 to correct PF field.)
XX Sequence 215 AA;
SQ

Alignment Scores: 5.49e-39 Length: 215
Pred. No.: 451.00 Matches: 91
Score: 83.62% Conservative: 6
Percent Similarity: 78.45% Mismatches: 17
Best Local Similarity: 66.91% Indels: 2
Query Match: 2 Gaps: 1
DB: 1

US-10-049-868A-1 (1-359) x AAR99644 (1-215)

QY 10 CTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGC 69
Db 4 LeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMetThrCys 23

QY 70 AGTGCCAGTCAAGTGTT-----AATTACATGCACTGGTTCCAGCAGGAGTCGGGCACC 123
Db 24 ArgAlaSerSerValSerSerTyrLeuHisTrpPheGlnGlnLysSerGlyAla 43

QY 124 TTCCCCAAAAGAGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db 44 SerProLysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProAlaArgPhe 63

QY 184 AGTGGCAGTGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTGAGGAT 243
Db 64 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerValGluAlaGluAsp 83

QY 244 GTGGGTGTGTTACTGTCAACAACTTGAGAGTATCCGCTCACGTTCCGTTGCTGGGACC 303
Db 84 AlaAlaThrTyrTyrCysGlnGlnTyrSerGlyTyrProLeuThrPheGlyAlaGlyThr 103

QY 304 AAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db 104 LysLeuGluLeuLysArgAlaAspAlaProThrValSerIlePhe 119

RESULT 10
AAR97377
ID AAR97377 standard; protein; 215 AA.
XX AAR97377;
AC AAR97377;
XX 25-MAR-2003 (revised)
DT 13-NOV-1996 (first entry)
XX
DE Murine anti-BGH MAB light chain.
XX
KW Antibody engineering; monoclonal antibody; MAB; light chain;
KW single chain antibody; immunoassay; bovine growth hormone; BGH.
XX Mus musculus.
OS
PN US5518889-A.
XX
PD 21-MAY-1996.
XX
PF 06-JUN-1995; 95US-00468988.
XX

PR 02-SEP-1986; 86US-00902971.
PR 02-SEP-1987; 87US-00092110.
PR 19-JAN-1989; 89US-00299617.
PR 25-APR-1990; 90US-00512910.
PR 01-APR-1993; 93US-00040440.
XX
PA (ENZO-) ENZON LABS INC.
XX
PI Bird RE, Ladner RC, Hardman K;
XX
DR WPI; 1996-259060/26.
DR N-PSDB; AAT29057.
XX
PT Immunoassay using single chain antigen binding mol. - as replacement for
PT labelled or immobilised antibody, are less immunogenic, easier to
PT engineer, more stable and less expensive.
XX
PS Example 1; Fig 22; 78pp; English.
XX
CC Portions of the heavy chain (AAR97376) and light chain (AAR97377) of
CC murine IgG1 anti-bovine growth hormone monoclonal antibody 3C2 can be
CC incorporated into novel single polypeptide chain binding molecules (see
CC also AAW02188-90). These are expressed in host cells using DNA constructs
CC (see also AAT36460-62) that include heavy and light chain encoding
CC sequences (AAT29056 and AAT29057) joined by linker moieties. Following
CC expression and refolding, the single chain binding molecules show the
CC binding characteristics of the aggregate of the 2 original heavy and
CC light chains of the variable region of the antibody. (Updated on 25-MAR-
CC 2003 to correct PF field.)
XX
SQ Sequence 215 AA;

Alignment Scores:

Pred. No.: 5.49e-39 Length: 215
Score: 451.00 Matches: 91
Percent Similarity: 83.62% Conservative: 6
Best Local Similarity: 78.45% Mismatches: 17
Query Match: 56.91% Indels: 2
DB: 2 Gaps: 1

US-10-049-868A-1 (1-359) x AAR97377 (1-215)

QY 10 CTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCCACCATGACCTGC 69
|||
Db 4 LeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMetThrCys 23

QY 70 AGTGCCAGTTCAGTGTT-----AATTACATGCACCTGGTTCCAGCAGGAGTCGGGCACC 123
|||
Db 24 ArgAlaSerSerSerValSerSerSerTyrLeuHisTrpPheGlnGlnLysSerGlyAla 43

QY 124 TTCCCCAAAGAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
|||
Db 44 SerProLysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProAlaArgphe 63

QY 184 AGTGGCAGTGGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTGAGGAT 243
|||
Db 64 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerValGluAlaGluAsp 83

QY 244 GTGGGTGTATTACTGTCAACAACCTGTGAGAGTATCCGCTCACGTTCCGTTGCTGGGACC 303
|||
Db 84 AlaAlaThrTyrTyrCysGlnGlnTyrSerGlyTyrProLeuThrPheGlyAlaGlyThr 103

QY 304 AAGCTGGAGCTGAACCGGCTGATGCTGCACCAACTGTATCCATCTTC 351
|||
Db 104 LysLeuGluLeuLysArgAlaAspAlaAlaProThrValSerIlePhe 119

RESULT 11

AAR21293

ID AAR21293 standard; protein; 108 AA.

XX

AC AAR21293;

XX

DT 21-MAY-1992 (first entry)

XX
DE
XX
KW
KW
XX
OS
XX
FH
FT
FT
FT
FT
FT
FT
XX
FN
XX
PD
XX
PF
XX
PR
PR
PR
PR
PR
PR
XX
PA
PA
XX
PI
PI
XX
DR
XX
PT
PT
PT
XX
PS
XX
CC
CC
CC
CC
CC
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CC
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CC
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CC
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CC
CC
CC
CC
CC
SQ

Murine VL kappa group IV/VI chain h specific for phOx.

Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
g3p; binding; adsorption; gene VIII; diverse repertoire;
specific binding pairs; replicable genetic display package.

Synthetic.

Key Location/Qualifiers
Binding-site 24..33
/label= CDR1
Binding-site 49..55
/label= CDR2
Binding-site 88..96
/label= CDR3
/note= " D-X-G-X-X motif "

WO9201047-A.

23-JAN-1992.

10-JUL-1990; 90GB-00015198.

10-JUL-1990; 90GB-00015198.

19-OCT-1990; 90GB-00022845.

12-NOV-1990; 90GB-00024503.

06-MAR-1991; 91GB-00004744.

15-MAY-1991; 91GB-00010549.

(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
(MEDI-) MED RES COUNCIL.

Mccafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
Jackson RH, Holliger KP, Marks JD;

WPI; 1992-056862/07.

Producing members of specific binding pairs - by expression in
recombinant host cells with a secreting replicable genetic display
package.

Example 22; Fig 24; 209pp; English.

The VK sequence is one of 23 (AAR21286-308) expressed from a single chain
Fv library. The library produces a diverse repertoire of antibody
fragments specific for 2-phenyl-5-oxazolone (phOx). It was prepd. using
cDNA generated from mRNA from mice immunised with phOx coupled to chicked
serum albumin. The VH and VL kappa sequences were separately amplified by
PCR (AAQ23474-84) and ligated into fdCAT2 (AAQ23463) for expression on
the phage surface as fusions with gene III. The resulting library of
clones was diverse; 23 hapten binding clones were sequenced revealing 8
VH genes (A-H; AAR21264-71) in a variety of pairings with 7 Vk genes (a-g
; AAR21286-92). Most clones were VH-B combinations so a further
hierarchical library was prepd. by "crossing" VH-B with the Vk
repertoire. The resulting library was screened for hapten binding and 24
clones sequenced. 14 new partners (AAR21293-308) for VH-B were
identified. Nearly all the Vk genes were "ox-like"; only f, (from the
original library) and h, p, q, and r (from the hierarchical library) were
Vkox1 type genes. Of the 24 hierarchical clones, 4 were of type "h". The
Kd of VH-B/Vk-d for phOx-GABA was 10 nM, one of the highest values found.
This suggests that phage bearing scFv fragments having weak affinities
can be selected with antigen, probably due to the avidity of the multiple
antibody heads on the phage. The different combinations could also be
isolated on a basis of antigen affinity. See also AAR21260-307, 309-311;
AAR22450, 565-581

Sequence 108 AA;

Alignment Scores:

Pred. No.: 1.02e-38 Length: 108
Score: 448.00 Matches: 87
Percent Similarity: 87.96% Conservative: 8

Best Local Similarity: 80.56% Mismatches: 13
Query Match: 66.47% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x AAR21293 (1-108)

QY 1 GACATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCACC 60
Db 1 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20

QY 61 ATGACCTGCAGTGCCAGTCAAGTGTAAATTACATGCACTGGTTCAGCAGGAGTGGGC 120
Db 21 MetThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGly 40

QY 121 ACCTTCCCCAAAAGAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 41 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArg 60

QY 181 CTCAGTGGCAGTGGGTCTGGGACAGAAATTCACCCCTGGAAATCAGTAGAGTGAGGCTGAG 240
Db 61 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80

QY 241 GATGTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCGCTCACGTTTCGGTGGG 300
Db 81 AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 100

QY 301 ACCAAGCTGGAGCTGAAACGGGCT 324
Db 101 ThrLysLeuGluIleLysArgAla 108

RESULT 12

AAR13060

ID AAR13060 standard; protein; 235 AA.

XX AC AAR13060;

XX 25-MAR-2003 (revised)

DT 03-OCT-1991 (first entry)

XX Monoclonal antibody OK3T light chain.

DE OK3T; light chain; humanised antibodies; CDR-grafting.

XX Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..22

FT /label= signal peptide

FT 23..235

FT /label= light chain

XX WO9109967-A.

XX 11-JUL-1991.

XX 21-DEC-1989; 89GB-00028874.

XX 21-DEC-1989; 89GB-00028874.

PR 21-DEC-1990; 90WO-GB002017.

XX (CLLT) CELLTech LTD.

XX Adair JR, Athwal DS, Emtage JS;

XX WPI; 1991-222915/30.

DR P-PSDB; AAR13060.

XX New humanised antibodies comprising CDR grafted antibody - with heavy and light chains, for use in vivo therapy and diagnosis.

PT Disclosure; Fig 1b; 91pp; English.

XX The OK3T light chain sequence was deduced from the cDNA sequence isolated

CC from a library prepared from OK3T producing cells. The library was screened with a probe complementary to a region in the mouse kappa constant region. The OK3T sequence was used in CDR- grafting experiments to prepare humanised antibodies. NOTE: Data found in patent WO9109968 has been used to index this entry. (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 235 AA;

Alignment Scores:

Pred. No.: 2,41e-38 Length: 235

Score: 445.00 Matches: 87

Percent Similarity: 83.62% Conservative: 10

Best Local Similarity: 75.00% Mismatches: 19

Query Match: 66.02% Indels: 0

DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x AAR13060 (1-235)

QY 4 ATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCACCATG 63

Db 24 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43

QY 64 ACCTGCAGTGCCAGTCAAGTGTAAATTACATGCACTGGTTCAGCAGGAGTGGGCACC 123

Db 44 ThrCysSerAlaSerSerValSerTyrMetAsnTrpTyrGlnGlnLysSerGlyThr 63

QY 124 TTCCCCAAAAGAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183

Db 64 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaHisPhe 83

QY 184 AGTGGCAGTGGGTCTGGGACAGAAATTCACCCCTGGAAATCAGTAGAGTGAGGCTGAGGAT 243

Db 84 ArgGlySerGlySerGlyThrSerTyrSerLeuThrIleSerGlyMetGluAlaGluAsp 103

QY 244 GTGGGTGTGTATTACTGTCAACAACTTGTAGAGTATCCGCTCACGTTCCGTTGGTGCTGGGACC 303

Db 104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProPheThrPheGlySerGlyThr 123

QY 304 AAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351

Db 124 LysLeuGluIleAsnArgAlaAspThrAlaProThrValSerIlePhe 139

RESULT 13

ABR62010

ID ABR62010 standard; protein; 241 AA.

XX AC ABR62010;

XX 03-OCT-2003 (first entry)

DE Single-chain (scFv) antibody.

XX Transgenic; biomolecule; ATP; ADP; cytostatic; virucide; gene therapy; antisense therapy; scFv; antibody.

XX Synthetic.

XX EP1321524-A1.

XX 25-JUN-2003.

XX 19-DEC-2001; 2001EP-00130319.

XX 19-DEC-2001; 2001EP-00130319.

PA (DUER/) DUERING K.

PI Mahn A, Hantke S, Petsch D;

XX WPI; 2003-543829/52.

DR N-PSDB; ACC84876.

XX

PT Increasing the content of transgene-coded biomolecules in a plant or
PT animal, useful for producing proteins for diagnosing, preventing and/or
PT treating viral diseases and cancer, comprises changing the distribution
PT of ATP and/or ADP.

XX
PS Example 2; Fig 2; 18pp; English.

XX
CC The invention relates to increasing the content of one or more transgene-
CC coded biomolecules in an organism and involves changing the distribution
CC of ATP and/or ADP in cells of the organism. The yield of transgenic
CC molecules in host cells is often insufficient for industrial production.
CC The method increases the yield of transgenic molecules in animal and
CC plant host cells, therefore facilitating their production on an
CC industrial scale. The proteins produced by the method are useful for
CC diagnosing, preventing and/or treating viral diseases and cancer. The
CC present sequence represents a single-chain (scFv) antibody, used to
CC exemplify the increase in the expression of scFv antibodies in transgenic
CC potato tubers

XX
SQ Sequence 241 AA;

Alignment Scores:
Pred. No.: 3.09e-38 Length: 241
Score: 444.00 Matches: 88
Percent Similarity: 86.36% Conservative: 7
Best Local Similarity: 80.00% Mismatches: 15
Query Match: 65.88% Indels: 0
DB: 6 Gaps: 0

US-10-049-868A-1 (1-359) x ABR62010 (1-241)

QY 1 GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCACC 60
Db 132 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 151

QY 61 ATGACCTGCAGTCCAGTTC AAGTGTAAATACATGCAC TGGTTCACAGCAGGAGTCGGGC 120
Db 152 MetThrCysSerAlaSerSerValArgTyrMetAsnTrpPheGlnGlnLysSerGly 171

QY 121 ACCTTCCCCAAAGAAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 172 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuSerSerGlyValProAlaArg 191

QY 181 CTCAGTGGCGTGTACTGTCAACAAC TTTGAGAGTATCCGCTCACGTCGAGGCTGAG 240
Db 212 AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 231

QY 301 ACCAAGCTGGAGCTGAAACGGGCTGATGCT 330
Db 232 ThrLysLeuGluLeuLysArgAlaAlaAla 241

RESULT 14
AAB11398
ID AAB11398 standard; protein; 255 AA.
XX
AC AAB11398;
XX
DT 22-FEB-2001 (first entry)

DE E. coli expression plasmid pUBS520-ScFvOx encoded protein.
XX
KW Eukaryotic protein; protease; interferon; antibody; hormone;
XX disulfide bridge.
OS Escherichia coli.
OS Synthetic.
XX
PN EP1048732-A1.
XX

PD 02-NOV-2000.
XX
PF 26-APR-1999; 99EP-00107412.
XX
PR 26-APR-1999; 99EP-00107412.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
DR WPI; 2000-674185/66.
DR N-PSDB; AAC66074.
XX
PT Preparation of water-soluble eukaryotic polypeptides with disulfide
PT bridges e.g. rPA, comprises cultivation of prokaryotic cells in the
PT presence of arginine or amide compound.
XX
PS Example 6; Page 22-23; 40pp; German.
XX
CC This invention describes a novel preparation of a water-soluble,
CC naturally occurring eukaryotic polypeptide containing two or more
CC cysteine units bound via a disulfide bridge which comprises cultivation
CC of prokaryotic cells in the presence of arginine or an amide compound.
CC The method is useful for the preparation of eukaryotic proteins e.g.
CC proteases, interferons, protein hormones, antibodies or antibody
CC fragments (e.g. a single chain FV fragment that binds to thyroid
CC stimulating hormone). It is especially useful for preparing proteins with
CC more than five disulfide bridges, e.g. recombinant plasminogen activator
CC (rPA). The technique is simple and does not require in vitro after-
CC treatment, such as the removal of inclusion bodies, reduction or
CC naturization

XX
SQ Sequence 255 AA;

Alignment Scores:
Pred. No.: 3.12e-38 Length: 255
Score: 444.00 Matches: 88
Percent Similarity: 86.36% Conservative: 7
Best Local Similarity: 80.00% Mismatches: 15
Query Match: 65.88% Indels: 0
DB: 3 Gaps: 0

US-10-049-868A-1 (1-359) x AAB11398 (1-255)

QY 1 GACATTGAGTCCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCACC 60
Db 132 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 151

QY 61 ATGACCTGCAGTCCAGTTC AAGTGTAAATACATGCAC TGGTTCACAGCAGGAGTCGGGC 120
Db 152 MetThrCysSerAlaSerSerValArgTyrMetAsnTrpPheGlnGlnLysSerGly 171

QY 121 ACCTTCCCCAAAGAAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 172 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuSerSerGlyValProAlaArg 191

QY 181 CTCAGTGGCGTGTCTGGGACAGAAATTCACCCCTGGAATCAGTAGAGTGAAGGCTGAG 240
Db 192 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 211

QY 241 GATGTGGTGTGTATTACTGTCAACAAC TTTGAGAGTATCCGCTCACGTCGAGTGGG 300
Db 212 AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 231

QY 301 ACCAAGCTGGAGCTGAAACGGGCTGATGCT 330
Db 232 ThrLysLeuGluLeuLysArgAlaAlaAla 241

RESULT 15
AAB74199
ID AAB74199 standard; protein; 255 AA.
XX
AC AAB74199;
XX
DT 29-MAY-2001 (first entry)

XX PelB-scFvOxazolon fusion protein.
DE Molecular chaperone; PelB signal sequence; scFvOxazolon.
XX

OS Unidentified.

XX EP1077262-A1.

XX PD 21-FEB-2001.

XX PF 24-JUL-2000; 2000EP-00115839.

XX PR 29-JUL-1999; 99EP-00114811.

XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX PI Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;

XX DR WPI; 2001-246712/26.

XX N-PSDB; AAF77806.

PT Producing naturally folded eukaryotic proteins e.g. antibodies,
PT interferon, hormones or proteases that contain two or several cysteines
PT linked by disulfide bridges comprises co-expression of a molecular
PT chaperone.

XX PS Disclosure; Page 19; 35pp; English.

XX The present invention relates to a method for production of a naturally
CC folded eukaryotic protein containing two or more cysteines linked by
CC disulfide bridges. The method comprises co-expression and secretion into
CC the periplasm of a molecular chaperone via an expression vector coding
CC for the chaperone. The expression vector also encodes a signal sequence.
CC The method is useful for producing a naturally folded eukaryotic protein
CC such as an antibody, antibody fragment, interferon, protein hormone or a
CC protease containing two or several cysteines linked by disulfide bridges.
CC The present sequence is a fusion protein composed of the PelB signal
CC presence and ScFvOxazolon. This sequence was used in the method of the
CC present invention

XX SQ Sequence 255 AA;

Alignment Scores:

Pred. No.:	3.12e-38	Length:	255
Score:	444.00	Matches:	88
Percent Similarity:	86.36%	Conservative:	7
Best Local Similarity:	80.00%	Mismatches:	15
Query Match:	65.88%	Indels:	0
DB:	4	Gaps:	0

US-10-049-868A-1 (1-359) x AAB74199 (1-255)

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Db	132	AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr	151
QY	61	ATGACCTGCAGTCCAGTTCAGTGTTAATTACATGCACCTGGTTCACGAGGAGTCGGGC	120
Db	152	MetThrCysSerAlaSerSerSerValArgTyrMetAsnTrpPheGlnGlnLysSerGly	171
QY	121	ACCTTCCCCAAGAAGGATTATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC	180
Db	172	ThrSerProLysArgTrpIleTyrAspThrSerLysLeuSerSerGlyValProAlaArg	191
QY	181	CTCAGTGGCAGTGGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTGAG	240
Db	192	PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu	211
QY	241	GATGTGGGTGTGTATTACTGTCAACAACCTTGATAGAGTATCCGCTCACGTCGGTGGTGGG	300
Db	212	AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly	231

QY 301 ACCAAGCTGGAGCTGAAACGGGCTGATGCT 330
Db 232 ThrLysLeuGluLeuLysArgAlaAla 241

Search completed: October 13, 2004, 13:21:04
Job time : 84.0429 secs

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GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 13, 2004, 13:28:16 ; Search time 69.6122 Seconds
(without alignments)
3328.244 Million cell updates/sec

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Perfect score: 674
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1356558 seqs, 322682953 residues

Total number of hits satisfying chosen parameters: 2713116

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10049868@cgn_1_1_260@runat_13102004_132820_24900
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description

ALIGNMENTS

RESULT 1
US-10-410-907A-34
; Sequence 34, Application US/10410907A
; Publication No. US20030215880A1
; GENERAL INFORMATION:
; APPLICANT: Dennis R. Burton
; APPLICANT: R. Anthony Williamson
; APPLICANT: Gianluca Moroncini
; TITLE OF INVENTION: MOTIF-GRAFTED HYBRID POLYPEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 22908-1229
; CURRENT APPLICATION NUMBER: US/10/410,907A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/371,610
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D18 Light Chain

1	471	69.9	215	14	US-10-410-907A-34	Sequence 34, Appl
2	459	68.1	129	14	US-10-344-779-2	Sequence 2, Appli
3	459	68.1	129	16	US-10-738-809-2	Sequence 2, Appli
4	458	68.0	235	9	US-09-910-059-17	Sequence 17, Appl
5	452	67.1	108	16	US-10-803-622-251	Sequence 251, App
6	452	67.1	108	16	US-10-803-653-251	Sequence 251, App
7	448	66.5	108	16	US-10-803-622-243	Sequence 243, App
8	448	66.5	108	16	US-10-803-653-243	Sequence 243, App
9	446	66.2	108	16	US-10-803-622-241	Sequence 241, App
10	446	66.2	108	16	US-10-803-653-241	Sequence 241, App
11	445	66.0	235	10	US-09-795-515-5	Sequence 5, Appli
12	445	66.0	235	15	US-10-704-352-5	Sequence 5, Appli
13	445	66.0	235	15	US-10-704-071-5	Sequence 5, Appli
14	440	65.3	107	9	US-09-144-886-82	Sequence 82, Appli
15	440	65.3	107	9	US-09-144-886-83	Sequence 83, Appli
16	439	65.1	108	9	US-09-910-059-9	Sequence 9, Appli
17	439	65.1	108	16	US-10-803-622-253	Sequence 253, App
18	439	65.1	108	16	US-10-803-653-253	Sequence 253, App
19	436	64.7	108	16	US-10-803-622-242	Sequence 242, App
20	436	64.7	108	16	US-10-803-653-242	Sequence 242, App
21	432	64.1	107	16	US-10-632-706-79	Sequence 79, Appl
22	432	64.1	107	16	US-10-632-706-80	Sequence 80, Appli
23	432	64.1	108	9	US-09-976-787-8	Sequence 8, Appli
24	432	64.1	108	9	US-09-865-198-8	Sequence 8, Appli
25	432	64.1	240	9	US-09-976-787-28	Sequence 28, Appl
26	432	64.1	240	9	US-09-865-198-27	Sequence 27, Appl
27	432	64.1	669	9	US-09-807-721-2	Sequence 2, Appli
28	428	63.5	108	16	US-10-803-622-240	Sequence 240, App
29	428	63.5	108	16	US-10-803-653-240	Sequence 240, App
30	427	63.4	108	16	US-10-803-622-252	Sequence 252, App
31	427	63.4	110	16	US-10-803-653-252	Sequence 252, App
32	427	63.4	110	16	US-10-803-622-256	Sequence 256, App
33	427	63.4	110	16	US-10-803-653-256	Sequence 256, App
34	427	63.4	256	14	US-10-247-488-2	Sequence 2, Appli
35	427	63.4	258	14	US-10-247-488-4	Sequence 4, Appli
36	425	63.1	108	16	US-10-803-622-244	Sequence 244, App
37	425	63.1	108	16	US-10-803-653-244	Sequence 244, App
38	424	62.9	110	16	US-10-803-622-255	Sequence 255, App
39	424	62.9	110	16	US-10-803-653-255	Sequence 255, App
40	424	62.9	119	9	US-09-808-037-28	Sequence 28, Appl
41	424	62.9	119	14	US-10-162-889-28	Sequence 28, Appl
42	424	62.9	119	15	US-10-384-788-28	Sequence 28, Appl
43	424	62.9	119	15	US-10-618-856-26	Sequence 26, Appl
44	424	62.9	239	9	US-09-808-037-6	Sequence 6, Appli
45	424	62.9	239	14	US-10-162-889-6	Sequence 6, Appli

US-10-410-907A-34

Alignment Scores:
Pred. No.: 5e-40 Length: 215
Score: 471.00 Matches: 91
Percent Similarity: 85.47% Conservative: 9
Best Local Similarity: 77.78% Mismatches: 17
Query Match: 69.88% Indels: 0
DB: 14 Gaps: 0

US-10-049-868A-1 (1-359) x US-10-410-907A-34 (1-215)

QY 1 GACATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACC 60
Db : : : : :
QY 3 GluLeuValLeuThrGlnSerProAlaPheMetSerAlaSerProGlyGluLysValThr 22
Db : : : : :
QY 61 ATGACCTGCAGTCCAGTTCAAAGTGTAAATTACATGCACCTGGTTCCAGCAGGAGTCGGGC 120
Db 23 MetThrCysSerAlaSerSerValAsnTyrMetHisTrpTyrGlnGlnLysSerGly 42
: : : : :
QY 121 ACCTTCCCAAAAGAAGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 43 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArg 62
: : : : :
QY 181 CTCAGTGGCAGTGGGTCTGGGACAGAATTACCCCTGGAAATCAGTAGAGTGAAGGCTGAG 240
Db 63 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 82
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QY 241 GATGTGGGTGTATTACTGTCAACACACTGTAGAGTATCCGCTCAGGTTCCGTTGCTGGG 300
Db 83 AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProTyrThrPheGlyGlyGly 102
: : : : :
QY 301 ACCAAGCTGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db 103 ThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSerIlePhe 119
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RESULT 2

US-10-344-779-2
; Sequence 2, Application US/10344779
; Publication No. US20030211106A1
; GENERAL INFORMATION:
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TORNETTA, MARK A.
; APPLICANT: TRUNEH, ALEMSEGED
; APPLICANT: WATTAM, TREVOR A.
; TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: USEFUL IN TREATMENT OF RANK LIGAND MEDIATED DISORDERS
; FILE REFERENCE: GP50033
; CURRENT APPLICATION NUMBER: US/10/344,779
; CURRENT FILING DATE: 2003-02-17
; PRIOR APPLICATION NUMBER: PCT/US01/26161
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,524
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/230,639
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-344-779-2

Alignment Scores:
Pred. No.: 8.26e-39 Length: 129
Score: 459.00 Matches: 89
Percent Similarity: 86.21% Conservative: 11
Best Local Similarity: 76.72% Mismatches: 16
Query Match: 68.10% Indels: 0
DB: 14 Gaps: 0

US-10-049-868A-1 (1-359) x US-10-344-779-2 (1-129)

QY 4 ATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATG 63
Db 2 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 21
: : : : :
QY 64 ACCTGCAGTCCAGTTCAGTGTAAATTACATGCACCTGGTTCCAGCAGGAGTCGGGCACC 123
Db 22 ThrCysSerAlaSerSerSerValSerTyrMetTyrTrpTyrGlnGlnLysProGlySer 41
: : : : :
QY 124 TTCCCAAAAGAAGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db 42 SerProArgLeuLeuIleTyrAspThrSerAsnLeuAlaSerGlyValProValArgPhe 61
: : : : :
QY 184 AGTGGCAGTGGGTCTGGGACAGAATTACCCCTGGAAATCAGTAGAGTGAAGGCTGAGGAT 243
Db 62 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGluAsp 81
: : : : :
QY 244 GTGGGTGTATTACTGTCAACAACTTGTAGAGTATCCGCTCAGGTTCCGTTGCTGGGACC 303
Db 82 AlaAlaThrTyrTyrCysGlnGlnTrpSerAsnPheProLeuThrPheGlyAlaGlyThr 101
: : : : :
QY 304 AAGCTGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db 102 LysLeuGluLeuLysArgAlaAspAlaAlaProThrValSerIlePhe 117
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RESULT 3

US-10-738-809-2
; Sequence 2, Application US/10738809
; Publication No. US20040171117A1
; GENERAL INFORMATION:
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TORNETTA, MARK A.
; APPLICANT: TRUNEH, ALEMSEGED
; APPLICANT: WATTAM, TREVOR A.
; TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: USEFUL IN TREATMENT OF RANK LIGAND MEDIATED DISORDERS
; FILE REFERENCE: GP50033
; CURRENT APPLICATION NUMBER: US/10/738,809
; CURRENT FILING DATE: 2003-12-17
; PRIOR APPLICATION NUMBER: US/10/344,779
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: PCT/US01/26161
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,524
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/230,639
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-738-809-2

Alignment Scores:
Pred. No.: 8.26e-39 Length: 129
Score: 459.00 Matches: 89
Percent Similarity: 86.21% Conservative: 11
Best Local Similarity: 76.72% Mismatches: 16
Query Match: 68.10% Indels: 0
DB: 16 Gaps: 0

US-10-049-868A-1 (1-359) x US-10-738-809-2 (1-129)

QY 4 ATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATG 63
Db 2 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 21
: : : : :
QY 64 ACCTGCAGTCCAGTTCAGTGTAAATTACATGCACCTGGTTCCAGCAGGAGTCGGGCACC 123
Db 22 ThrCysSerAlaSerSerValSerTyrMetTyrTrpTyrGlnGlnLysProGlySer 41
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RESULT 4

QY 124 TTCCCAAAGAAGGATTATGACACATCCAAAACGGTCTTCTGGAGTCCCTGCTCGCCTC 183
Db 42 SerProArgLeuLeuIleTyrAspThrSerAsnLeuAlaSerGlyValProValArgPhe 61
QY 184 AGTGGCAGTGGTCTGGACAGAAATTCACCCCTGGAAATCAGTAGAGTGAAGGCTGAGGAT 243
Db 62 SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGluAsp 81
QY 244 GTGGGTGTGTATTACTGTCAACAACCTTGATAGAGTATCCGCTCACGTTCCGTTGCTGGGACC 303
Db 82 AlaAlaThrTyrTyrCysGlnGlnTrpSerAsnPheProLeuThrPheGlyAlaGlyThr 101
QY 304 AAGCTGGAGCTGAAACGGGCTGATGTGTCACCAACTGTATCCATCTTC 351
Db 102 LysLeuGluLeuLysArgAlaAspAlaProThrValSerIlePhe 117
RESULT 4
US-09-910-059-17
; Sequence 17, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 17
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimaeric light chain sequence
US-09-910-059-17

Alignment Scores:
Pred. No.: 1.12e-38 Length: 235
Score: 458.00 Matches: 90
Percent Similarity: 83.76% Conservative: 8
Best Local Similarity: 76.92% Mismatches: 19
Query Match: 67.95% Indels: 0
DB: 9 Gaps: 0
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QY 1 GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAAGGTCACC 60
Db 23 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 42
QY 61 ATGACCTGCAGTCCAGTTCAAGTGTTAATTACATGCACCTGGTTCCAGCAGGAGTCGGGC 120
Db 43 IleThrCysSerAlaSerSerSerValThrTyrMetHisTrpPheGlnGlnLysProGly 62
QY 121 ACCTTCCCAAAGAAGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 63 ThrSerProLysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProAlaArg 82
QY 181 CTCAGTGGCAGTGGTCTGGGACAGAAATTCACCCCTGGAAATCAGTAGAGTGAAGGCTGAG 240
Db 83 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGlu 102

QY 241 GATGTGGGTGTATTACTGTCAACAACCTTGATAGAGTATCCGCTCACGTTCCGTTGCTGGG 300
Db 103 AspAlaAlaThrTyrTyrCysGlnGlnArgSerThrTyrProLeuThrPheGlyAlaGly 122
QY 301 ACCAAGCTCGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db 123 ThrLysLeuGluIleLysArgThrValAlaAlaProSerValPheIlePhe 139
RESULT 5
US-10-803-622-251
; Sequence 251, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,622
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 251
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-251

Alignment Scores:
Pred. No.: 4.3e-38 Length: 108
Score: 452.00 Matches: 88
Percent Similarity: 88.89% Conservative: 8
Best Local Similarity: 81.48% Mismatches: 12
Query Match: 67.06% Indels: 0
DB: 16 Gaps: 0
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QY 1 GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAAGGTCACC 60
Db 1 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20

QY	61	ATGACCTGCAGTGCCAGTTCAAAGTGTTAATTACATGCACCTGGTTCCAGCAGGAGT	CGGGC	120
Dd	21	MetThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGly	40	
QY	121	ACCTTCCCCAAAAGAAGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC	180	
Dd	41	ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArg	60	
QY	181	CTCAGTGGCAGTGGGTCTGGGACAGAAATTCACCCCTGGAATCAGTAGAGTGAAGCTGAG	240	
Dd	61	PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu	80	
QY	241	GATGTGGGTGTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTCCGTGCTGGG	300	
Dd	81	AspValAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly	100	
QY	301	ACCAAGCTGGAGCTGAAACGGGCT	324	
Dd	101	ThrLvsLeuGluileLvsArgAla	108	

RESULT 6

```

US-10-803-653-251
; Sequence 251, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,653
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 251
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazol
US-10-803-653-251

```

```

Alignment Scores:
Pred. No.: 4.3e-38 Length: 108
Score: 452.00 Matches: 88
Percent Similarity: 88.89% Conservative: 8
Best Local Similarity: 81.49% Mismatches: 12
Query Match: 67.06% Indels: 0
DB: 16 Gaps: 0

US-10-049-868A-1 (1-359) x US-10-803-653-251 (1-108)

QY 1 GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCAAC 60
Db 1 AspileGluLeuThrGlnSerProAlaileMetSerAlaSerProGlyGluLysValThr 20
QY 61 ATGACCTGCAGTGCCAGTTCAGTGTAAATTACATGCACCTGGTTCCAGCAGGAGTCGGGC 120
Db 21 MetThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGly 40
QY 121 ACCTTCCCCAAAAGAGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 41 ThrSerProLysArgTrpileTyrAspThrSerLysLeuAlaSerGlyValProAlaArg 60
QY 181 CTCAGTGGCAGTGGGTCTGGGACAGAATTACCCCTGGAAATCAGTAGAGTCAAGGCTGAG 240
Db 61 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80
QY 241 GATGTGGTGTGTATTACTGTCAACAACCTGTAGAGTATCCGCTCACGTTCCGTGCTGGG 300
Db 81 AspValAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 100
QY 301 ACCAAGCTGGAGCTGAAACGGGCT 324
Db 101 ThrLysLeuGluIleLysArgAla 108

RESULT 7
US-10-803-622-243
; Sequence 243, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hocgenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,622
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857

```



```
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 243
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-243

Alignment Scores:
Pred. No.:      1.12e-37      Length:      108
Score:          448.00      Matches:      87
Percent Similarity: 87.96%      Conservative: 8
Best Local Similarity: 80.56%      Mismatches: 13
Query Match:    66.47%      Indels:      0
DB:             16      Gaps:      0

US-10-049-868A-1 (1-359) x US-10-803-622-243 (1-108)

QY      1  GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACC 60
      |||||||
Db      1  AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20

QY      61  ATGACCTGCAGTGCAGTTCAAGTGTAAATTACATGCACCTGGTTCACGAGGAGTCGGGC 120
      |||||||
Db      21  MetThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGly 40

QY      121  ACCTTCCCCAAAAGAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
      |||
Db      41  ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArg 60

QY      181  CTCAGTGGCAGTGGTCTGGGACAGAATTACCCCTGGAAATCAGTAGAGTGAAGGCTGAG 240
      |||||||
Db      61  PheSerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80

QY      241  GATGTGGGTGTATTACTGTCAACAACCTTGATAGAGTATCCGCTCACGTTCCGGTGTGGG 300
      |||
Db      81  AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 100

QY      301  ACCAAGCTGGAGCTGAAACGGGCT 324
      |||
Db      101  ThrLysLeuGluIleLysArgAla 108

RESULT 8
US-10-803-653-243
; Sequence 243, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,653
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
```

```
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 243
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-243

Alignment Scores:
Pred. No.:      1.12e-37      Length:      108
Score:          448.00      Matches:      87
Percent Similarity: 87.96%      Conservative: 8
Best Local Similarity: 80.56%      Mismatches: 13
Query Match:    66.47%      Indels:      0
DB:             16      Gaps:      0

US-10-049-868A-1 (1-359) x US-10-803-653-243 (1-108)

QY      1  GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACC 60
      |||||||
Db      1  AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20

QY      61  ATGACCTGCAGTGCAGTTCAAGTGTAAATTACATGCACCTGGTTCACGAGGAGTCGGGC 120
      |||||||
Db      21  MetThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGly 40

QY      121  ACCTTCCCCAAAAGAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
      |||
Db      41  ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArg 60

QY      181  CTCAGTGGCAGTGGTCTGGGACAGAATTACCCCTGGAAATCAGTAGAGTGAAGGCTGAG 240
      |||||||
Db      61  PheSerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80

QY      241  GATGTGGGTGTATTACTGTCAACAACCTTGATAGAGTATCCGCTCACGTTCCGGTGTGGG 300
      |||
Db      81  AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 100

QY      301  ACCAAGCTGGAGCTGAAACGGGCT 324
      |||
Db      101  ThrLysLeuGluIleLysArgAla 108

RESULT 9
US-10-803-622-241
; Sequence 241, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
```

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; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,622
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-241

Alignment Scores:
Pred. No.: 1.8e-37 Length: 108
Score: 446.00 Matches: 87
Percent Similarity: 87.04% Conservative: 7
Best Local Similarity: 80.56% Mismatches: 14
Query Match: 66.17% Indels: 0
DB: 16 Gaps: 0

US-10-049-868A-1 (1-359) x US-10-803-622-241 (1-108)
QY 1 GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACC 60
Db 1 AspileGluLeuThrGlnSerProAlaIleMetSerAlaPheProGlyGluLysValThr 20

QY 61 ATGACCTGCAGTGCCAGTTCAGTGTAAATTACATGCACCTGGTTCAGCAGGAGTCGGGC 120
Db 21 MetThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGly 40

QY 121 ACCTTCCCCAAAAGAGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 41 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArg 60

QY 181 CTCAGTGGCAGTGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTGAG 240
Db 61 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80

QY 241 GATGTGGGTGTATTACTGTCAACAACTTGTAGAGTATCCGCTCACGTTCCGGTCTGGG 300
Db 81 AspAlaAlaThrTyrTyrCysGlnGlnPheSerSerAsnProLeuThrPheGlyAlaGly 100

QY 301 ACCAAGCTGGAGCTGAAACGGGCT 324
Db 101 ThrLysLeuGluLeuLysArgAla 108
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RESULT 10
US-10-803-653-241
; Sequence 241, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,653
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-241

Alignment Scores:
Pred. No.: 1.8e-37 Length: 108
Score: 446.00 Matches: 87
Percent Similarity: 87.04% Conservative: 7
Best Local Similarity: 80.56% Mismatches: 14
Query Match: 66.17% Indels: 0
DB: 16 Gaps: 0

US-10-049-868A-1 (1-359) x US-10-803-653-241 (1-108)
QY 1 GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACC 60
Db 1 AspileGluLeuThrGlnSerProAlaIleMetSerAlaPheProGlyGluLysValThr 20

QY 61 ATGACCTGCAGTGCCAGTTCAGTGTAAATTACATGCACCTGGTTCAGCAGGAGTCGGGC 120
Db 21 MetThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGly 40

QY 121 ACCTTCCCCAAAAGAGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 41 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArg 60
```

QY 181 CTCAGTGGCAGTGGTCTGGGACAGAATTACCCCTGGAAATCAGTAGAGTGAAGGCTGAG 240
Db 61 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80
QY 241 GATGTGGGTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTCCGGTGGTGGG 300
Db 81 AspAlaAlaThrTyrTyrCysGlnGlnPheSerSerAsnProLeuThrPheGlyAlaGly 100
QY 301 ACCAAGCTGGAGCTGAACGGGCT 324
Db 101 ThrLysLeuGluLeuLysArgAla 108

RESULT 11
US-09-795-515-5
; Sequence 5, Application US/09795515
; Publication No. US20030039645A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US200030039645A1ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-795-515-5

Alignment Scores:
Pred. No.: 2.49e-37 Length: 235
Score: 445.00 Matches: 87
Percent Similarity: 83.62% Conservative: 10
Best Local Similarity: 75.00% Mismatches: 19
Query Match: 66.02% Indels: 0
DB: 10 Gaps: 0

US-10-049-868A-1 (1-359) x US-09-795-515-5 (1-235)

QY 4 ATTGAGCTACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCCACCATG 63
Db 24 IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43
QY 64 ACCTGCAGTCCAGTTCAAGTGTTAATTACATGCACCTGGTTCAGCAGGAGTCCGGGCACC 123

Db 44 ThrCysSerAlaSerSerValSerTyrMetAsnTrpTyrGlnGlnLysSerGlyThr 63
QY 124 TTCCCCAAAAGAGATTATGACACATCCAAAACCTGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db 64 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaHisPhe 83
QY 184 AGTGGCAGTGGTCTGGGACAGAATTACCCCTGGAATCAGTAGAGTGAAGGCTGAGGAT 243
Db 84 ArgGlySerGlySerGlyThrSerTyrSerLeuThrIleSerGlyMetGluAlaGluAsp 103
QY 244 GTGGGTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTCCGGTGGGACC 303
Db 104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnPropheThrPheGlySerGlyThr 123
QY 304 AAGCTGGAGCTGAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db 124 LysLeuGluIleAsnArgAlaAspThrAlaProThrValSerIlePhe 139

RESULT 12
US-10-704-352-5
; Sequence 5, Application US/10704352
; Publication No. US20040071693A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/704,352
; FILING DATE: 07-Nov-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE: 28-FEB-2001
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-704-352-5

Alignment Scores:
Pred. No.: 2.49e-37 Length: 235
Score: 445.00 Matches: 87
Percent Similarity: 83.62% Conservative: 10
Best Local Similarity: 75.00% Mismatches: 19
Query Match: 66.02% Indels: 0
DB: 15 Gaps: 0

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US-10-049-868A-1 (1-359) x US-10-704-352-5 (1-235)
QY 4 ATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAAGGTCAACCATG 63
Db 24 IlevallLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43
QY 64 ACCTGCAGTCCAGTTCAAGTGTTAATTACATGCACCTGGTTCACAGGAGTCCGGGCACC 123
Db 44 ThrCysSerAlaSerSerValSerTyrMetAsnTrpTyrGlnGlnLysSerGlyThr 63
QY 124 TTCCCCAAAAGAAGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db 64 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaHisPhe 83
QY 184 AGTGGCAGTGGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTGAGGAT 243
Db 84 ArgGlySerGlySerGlyThrSerTyrSerLeuThrIleSerGlyMetGluAlaGluAsp 103
QY 244 GTGGGTGTGTATTACTGTCAACAACCTGTAGAGTATCCGCTCACGTTCCGGTGGGACC 303
Db 104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProPheThrPheGlySerGlyThr 123
QY 304 AAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db 124 LysLeuGluIleAsnArgAlaAspThrAlaProThrValSerIlePhe 139

RESULT 13
US-10-704-071-5
; Sequence 5, Application US/10704071
; Publication No. US20040076627A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; Athwal, Diljeet S.
; Entage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/704,071
; FILING DATE: 07-Nov-2003
; CLASSIFICATION: (D)
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-704-071-5
Alignment Scores:
Pred. No.: 2.49e-37 Length: 235
Score: 445.00 Matches: 87
Percent Similarity: 83.62% Conservative: 10
Best Local Similarity: 75.00% Mismatches: 19
Query Match: 66.02% Indels: 0
DB: 15 Gaps: 0

US-10-049-868A-1 (1-359) x US-10-704-071-5 (1-235)
QY 4 ATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAAGGTCAACCATG 63
Db 24 IlevallLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43
QY 64 ACCTGCAGTCCAGTTCAGTGTTAATTACATGCACCTGGTTCACAGGAGTCCGGGCACC 123
Db 44 ThrCysSerAlaSerSerValSerTyrMetAsnTrpTyrGlnGlnLysSerGlyThr 63
QY 124 TTCCCCAAAAGAAGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db 64 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaHisPhe 83
QY 184 AGTGGCAGTGGGTCTGGGACAGAAATTCACCTGGAAATCAGTAGAGTGAAGGCTGAGGAT 243
Db 84 ArgGlySerGlySerGlyThrSerTyrSerLeuThrIleSerGlyMetGluAlaGluAsp 103
QY 244 GTGGGTGTGTATTACTGTCAACAACCTGTAGAGTATCCGCTCACGTTCCGGTGGGACC 303
Db 104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProPheThrPheGlySerGlyThr 123
QY 304 AAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db 124 LysLeuGluIleAsnArgAlaAspThrAlaProThrValSerIlePhe 139

RESULT 14
US-09-144-886-82
; Sequence 82, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone
; OTHER INFORMATION: 1E8 region VL epitope 1
US-09-144-886-82
Alignment Scores:
Pred. No.: 7.51e-37 Length: 107
Score: 440.00 Matches: 86
Percent Similarity: 86.92% Conservative: 7
Best Local Similarity: 80.37% Mismatches: 14
Query Match: 65.28% Indels: 0
DB: 9 Gaps: 0

US-10-049-868A-1 (1-359) x US-09-144-886-82 (1-107)
QY 1 GACATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAAGGTCAACC 60
Db 1 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValIle 20
QY 61 ATGACCTGCAGTCCAGTTCAGTGTTAATTACATGCACCTGGTTCACAGGAGTCCGGGC 120
Db 21 MetThrCysSerAlaSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGly 40
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```
QY      121  ACCTTCCCCAAAGAAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db      41  ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArg 60

QY      181  CTCAGTGGCAGTGGGTCTGGGACAGAATTACCCCTGGAAATCAGTAGAGTGAAGGCTGAG 240
Db      61  PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80

QY      241  GATGTGGGTGTGTATTACTGTCAACAACATTGTAGAGTATCCGCTCACGTTCCGTTGCTGGG 300
Db      81  AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 100

QY      301  ACCAAGCTGGAGCTGAAACGG 321
Db      101 ThrLysLeuGluLeuLysArg 107
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RESULT 15
US-09-144-886-83
; Sequence 83, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone
; OTHER INFORMATION: 1G7 region VL epitope 1
US-09-144-886-83
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Alignment Scores:
Pred. No.:      7.51e-37      Length:      107
Score:          440.00      Matches:      86
Percent Similarity: 86.92%      Conservative: 7
Best Local Similarity: 80.37%      Mismatches: 14
Query Match:     65.28%      Indels:    0
DB:              9          Gaps:      0
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US-10-049-868A-1 (1-359) x US-09-144-886-83 (1-107)

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Db      1  AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValIle 20

QY      61  ATGACCTGCAGTGCCAGTTCAGTGTTAATTACATGCACCTGGTTCCAGCAGGAGTCGGGC 120
Db      21  MetThrCysSerAlaSerSerSerValSerTyrMetHisTrpTyrGlnGlnLysSerGly 40

QY      121  ACCTTCCCCAAAGAAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db      41  ThrSerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaArg 60

QY      181  CTCAGTGGCAGTGGGTCTGGGACAGAATTACCCCTGGAAATCAGTAGAGTGAAGGCTGAG 240
Db      61  PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 80

QY      241  GATGTGGGTGTGTATTACTGTCAACAACATTGTAGAGTATCCGCTCACGTTCCGGTGTGGG 300
Db      81  AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 100

QY      301  ACCAAGCTGGAGCTGAAACGG 321
Db      101 ThrLysLeuGluLeuLysArg 107
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Search completed: October 13, 2004, 13:53:40
Job time : 71.6122 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 13, 2004, 13:12:25 ; Search time 21.6191 Seconds
(without alignments)
3231.093 Million cell updates/sec

Title: US-10-049-868A-2
Perfect score: 673
Sequence: 1 cagggtcagctgcaggagtc.....ccacggtcaccgtctctctca 363

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2 1/USPTO_spool_p/US10049868/runat 13102004 132817 24805/app_query.fasta 1.1038
-DB=PIR_79 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10049868 @CGN 1 1 77 @runat 13102004 132817 24805 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	552.5	82.1	141	2 S52446	Ig heavy chain V r
2	536	79.6	112	2 S11100	Ig heavy chain V r
3	533.5	79.3	117	2 S38563	Ig heavy chain V r
4	530.5	78.8	120	2 PL0087	Ig heavy chain V r
5	529	78.6	140	2 S55028	Ig heavy chain V r
6	527	78.3	113	2 S11101	Ig heavy chain V r
7	527	78.3	114	2 S11106	Ig heavy chain V r
8	527	78.3	116	2 S11102	Ig heavy chain V r
9	524.5	77.9	139	2 A32456	Ig heavy chain pre
10	521	77.4	112	2 S11108	Ig heavy chain V r
11	517	76.8	115	2 S11103	Ig heavy chain V r
12	515	76.5	114	2 S11099	Ig heavy chain V r
13	507.5	75.4	116	2 S42484	Ig heavy chain V r
14	500.5	74.4	122	2 A49049	Ig heavy chain V r

15	500	74.3	106	2 S26322	Ig heavy chain V r
16	499	74.1	118	2 PQ0266	Ig heavy chain V r
17	497.5	73.9	135	2 S31913	Ig gamma-2A chain
18	492.5	73.2	122	2 S20809	Ig heavy chain V r
19	492	73.1	106	2 S14489	Ig heavy chain V r
20	492	73.1	114	2 S11105	Ig heavy chain V r
21	491	73.0	112	2 S11098	Ig heavy chain V r
22	490	72.8	117	2 S10111	Ig heavy chain V r
23	489	72.7	140	2 S14238	Ig gamma-1 chain p
24	487	72.4	127	2 B31807	Ig heavy chain V r
25	487	72.4	144	1 G2MS14	Ig heavy chain pre
26	486.5	72.3	118	2 S32786	Ig heavy chain (an
27	483	71.8	121	2 D30560	Ig heavy chain V r
28	480	71.3	121	2 S33131	Ig heavy chain V r
29	480	71.3	231	2 PC4155	Ig heavy chain V r
30	479	71.2	109	2 S11109	Ig gamma-2b chain
31	479	71.2	114	2 S11104	Ig heavy chain V r
32	478.5	71.1	144	2 S11244	Ig gamma-2a chain
33	477	70.9	107	2 S14492	Ig heavy chain V r
34	476	70.7	107	2 S14493	Ig heavy chain V r
35	475	70.6	100	2 S14490	Ig heavy chain V r
36	473	70.3	115	2 S11107	Ig heavy chain V r
37	471	70.0	111	2 S26324	Ig heavy chain V r
38	471	70.0	114	2 S26321	Ig heavy chain V r
39	470	69.8	107	2 S14491	Ig heavy chain V r
40	467.5	69.5	110	2 PH1024	Ig heavy chain V r
41	467	69.4	95	2 S17605	Ig heavy chain V r
42	464	68.9	110	2 S26323	Ig heavy chain V r
43	463	68.8	109	2 PH1025	Ig heavy chain V r
44	461.5	68.6	115	2 S26470	Ig heavy chain V r
45	455	67.6	101	2 S03466	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S52446
Ig heavy chain V region precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 03-Aug-1995 #text_change 23-Jul-1999
C;Accession: S52446
R;Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of rearranged germline DNA
A;Reference number: S52445
A;Accession: S52446
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-141 <BER>
A;Cross-references: EMBL:X82692; NID:g673441; PIDN:CAA58013.1; PID:g673442
C;Genetics:
A;introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 1.06e-46 Length: 141
Score: 552.50 Matches: 109
Percent Similarity: 90.98% Conservative: 2
Best Local Similarity: 89.34% Mismatches: 10
Query Match: 82.10% Indels: 1
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x S52446 (1-141)

QY	1	CAGGTGCAGCTGCAGGAGTCTGGACCTGGTGGCGCCTCACAGAGCCTGTCCATC	60
Db	20	GlnValGlnLeuLysGlnSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle	39
QY	61	ACTTGCACTGTCTCTGGGATTTCATTAAACAGATATGGTGTACACTGGTTCGCCAGCCT	120
Db	40	ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro	59

Score: 530.50 Matches: 104
Percent Similarity: 88.43% Conservative: 3
Best Local Similarity: 85.95% Mismatches: 13
Query Match: 78.83% Indels: 1
DB: 2 Gaps: 1
US-10-049-868A-2 (1-363) x PL0087 (1-120)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 1 GlnValGlnLeuLysArgSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20

QY 61 ACTTGCACTGTCTCTGGGATTTTCATTAAACAGATATGGTGATACACTGGGTTCGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerSerGlyValHisTrpValArgGlnPro 40

QY 121 CCAGGAAAGGTCGAGTGGCTGGGAGTAATATGGACTGGTGAAGCACAAATATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60

QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCAAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuThrIleSerLysAspAsnSerLysSerGlnValPheLeu 80

QY 241 AAAATGAACAGCTGCAGACTGATGACACAGCCATGTACTGTGCCAGATCGATCT 300
Db 81 LysMetThrSerLeuGlnIleAspAspThrAlaMetTyrTyrCysAlaArgAsp--Ser 99

QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCCAAGGACCAAGTCCACCGTCTCC 360
Db 100 HisCysGlyGlnAlaTyrGlyMetAspTyrTrpGlyGlnGlyThrSerValThrValSer 119

QY 361 TCA 363
Db 120 Ser 120

RESULT 5
S55028
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 23-Jul-1999
C;Accession: S55028
R;Jeffrey, P.D.; Schildbach, J.F.; Chang, C.Y.; Kussie, P.H.; Margolies, M.N.; Sheriff, J. Mol. Biol. 248, 344-360, 1995
A;Title: Structure and specificity of the anti-digoxin antibody 40-50.
A;Reference number: S55027; MUID:95257394; PMID:7739045
A;Accession: S55028
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <JEFF>
A;Cross-references: EMBL:L31403; NID:g476717; PIDN:AAA38191.1; PID:g476718
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 2.27e-44 Length: 140
Score: 529.00 Matches: 100
Percent Similarity: 88.43% Conservative: 7
Best Local Similarity: 82.64% Mismatches: 14
Query Match: 78.60% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-2 (1-363) x S55028 (1-140)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 20 GlnValHisLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 39

QY 61 ACTTGCACTGTCTCTGGGATTTTCATTAAACAGATATGGTGATACACTGGGTTCGCCAGCCT 120
Db 40 ThrCysThrValSerGlyPheSerLeuThrThrTyrGlyValHisTrpPheArgGlnPro 59

QY 121 CCAGGAAAGGTCCTGGAGTGGCTGGGAGTAATATATGGACTGGTGAAGCACAAATATAAT 180
Db 60 ProGlyLysGlyLeuGluTrpLeuGlyLeuIleTrpAlaGlyGlyAsnThrAspTyrAsn 79

QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCAAAGTTTCTTA 240
Db 80 SerAlaLeuMetSerArgLeuSerIleAsnLysAspAsnSerLysSerGlnValPheLeu 99

QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGATCGATCT 300
Db 100 LysMetAsnSerLeuGlnAlaAspAspThrAlaMetTyrTyrCysAlaArgPheArgPhe 119

QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCCAAGGACCAAGTCCACCGTCTCC 360
Db 120 AlaSerTyrTyrAspTyrAlaValAspTyrTrpGlyGlnGlyThrSerValThrValSer 139

QY 361 TCA 363
Db 140 Ser 140

RESULT 6
S11101
Ig heavy chain V region (clone NQ2-48.2.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C;Accession: S11101
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C. Nature 304, 320-324, 1983
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A;Reference number: S07331; MUID:83271467; PMID:6877353
A;Accession: S11101
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <KAA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 3.59e-44 Length: 113
Score: 527.00 Matches: 102
Percent Similarity: 85.95% Conservative: 2
Best Local Similarity: 84.30% Mismatches: 9
Query Match: 78.31% Indels: 8
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x S11101 (1-113)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuVal**ProSerGlnSerLeuSerIle 20

QY 61 ACTTGCACTGTCTCTGGGATTTTCATTAAACAGATATGGTGATACACTGGGTTCGCCAGCCT 120
Db 21 ThrCysThrValSerGly**SerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40

QY 121 CCAGGAAAGGTCCTGGAGTGGCTGGGAGTAATATATGGACTGGTGAAGCACAAATATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60

QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCAAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSer**ValPheLeu 80

QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGATCGATCT 300
Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspArgGly 100

QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCCAAGGACCAAGTCCACCGTCTCC 360
Db 101 Val-----TyrTrpGlyGlnGlyThrLeuValThrValSer 112

QY 361 TCA 363
Db 363

Db 113 Ala 113

RESULT 7

S11106

Ig heavy chain V region (clone NQ5-96.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000

C;Accession: S11106

R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.

Nature 304, 320-324, 1983

A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone

A;Reference number: S07331; MUID:83271467; PMID:6877353

A;Accession: S11106

A;Molecule type: mRNA

A;Residues: 1-114 <NAT>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	3.59e-44	Length:	114
Score:	527.00	Matches:	102
Percent Similarity:	85.95%	Conservative:	2
Best Local Similarity:	84.30%	Mismatches:	9
Query Match:	78.31%	Indels:	8
DB:	2	Gaps:	1

US-10-049-868A-2 (1-363) x S11106 (1-114)

QY 1	CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTCCATC	60
Db 1	GlnValGlnLeuLysGlu**GlyProGlyLeuVal**ProSerGlnSerLeuSerIle	20
QY 61	ACTTGCACTGTCTCTGGGATTTCATTAAACAGATATGGTGTAACACTGGGTTCCGCCAGCCT	120
Db 21	ThrCysThrValSerGly**SerLeuThrSerTyrGlyValHisTrpValArgGlnPro	40
QY 121	CCAGGAAGGGTCTGGAGTGGCTGGAGTAATATGGAGTAAACAGATATGGTGTAACACTGGGTTCCGCCAGCCT	180
Db 41	ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn	60
QY 181	TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAAGAGCCAAAGTTTCTTA	240
Db 61	SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu	80
QY 241	AAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT	300
Db 81	LysMetAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAspArgGly	100
QY 301	ACTATGATTACGGCCTATGCTATGGACTACTGGGCGCAAGGACCCACGGTCACCGTCTCC	360
Db 99	-----GlyPheAlaTyrTrpGlyGlnGlyThrSerValThrValSer	112
QY 361	TCA 363	
Db 113	Ser 113	

RESULT 8

S11102

Ig heavy chain V region (clone NQ5-4.3.1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000

C;Accession: S11102

R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.

Nature 304, 320-324, 1983

A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone

A;Reference number: S07331; MUID:83271467; PMID:6877353

A;Accession: S11102

A;Molecule type: mRNA

A;Residues: 1-116 <NAT>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	6.33e-44	Length:	139
Score:	524.50	Matches:	102
Percent Similarity:	89.17%	Conservative:	5
Best Local Similarity:	85.00%	Mismatches:	12
Query Match:	77.93%	Indels:	1
DB:	2	Gaps:	1

US-10-049-868A-2 (1-363) x A32456 (1-139)

QY 4	GTGCAGCTGCAGGAGTCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACT	63
Db 21	ValHisLeuLysGluSerGlyProValLeuValAlaProSerGlnSerLeuSerIleThr	40
QY 64	TGCACGTGCTCTGGGATTTCATTAAACAGATATGGTGTAACAGATATGGTTCGCCAGCCTCCA	123

Pred. No.: 3.58e-44 Length: 116

Score: 527.00 Matches: 102

Percent Similarity: 85.95% Conservative: 2

Best Local Similarity: 84.30% Mismatches: 9

Query Match: 78.31% Indels: 8

DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x S11102 (1-116)

QY 1	CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTCCATC	60
Db 1	GlnValGlnLeuLysGluSerGlyProGlyLeuVal**ProSerGlnSerLeuSerIle	20
QY 61	ACTTGCACTGTCTCTGGGATTTCATTAAACAGATATGGTGTAACACTGGGTTCCGCCAGCCT	120
Db 21	ThrCysThrValSerGly**SerLeuThrSerTyrGlyValHisTrpValArgGlnPro	40
QY 121	CCAGGAAGGGTCTGGAGTGGCTGGAGTAATATGGAGTAAACAGATATGGTGTAACACTGGGTTCCGCCAGCCT	180
Db 41	ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn	60
QY 181	TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAAGAGCCAAAGTTTCTTA	240
Db 61	SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSer**ValPheLeu	80
QY 241	AAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT	300
Db 81	LysMetAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAspArgGly	100
QY 301	ACTATGATTACGGCCTATGCTATGGACTACTGGGCGCAAGGACCCACGGTCACCGTCTCC	360
Db 101	***-----TyrTrpGlyGlnGlyThrLeuValThrValSer	112
QY 361	TCA 363	
Db 113	Ala 113	

RESULT 9

A32456

Ig heavy chain precursor V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 26-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999

C;Accession: A32456

R;Dombrink-Kurtzman, M.A.; Johnson, L.S.; Riordan, G.S.; Bedzyk, W.D.; Voss Jr., E.W.

J. Biol. Chem. 264, 4513-4522, 1989

A;Title: Variable region primary structures of a high affinity anti-fluorescein immunog

A;Reference number: A32456; MUID:89174706; PMID:2494173

A;Accession: A32456

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-139 <DOM>

A;Cross-references: GB:J04609; NID:G556316; PIDN:AAA50298.1; PID:G556317

A;Note: the authors translated the codon CAC for residue 20 as Gln, and CAC for residue

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-116/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	6.33e-44	Length:	139
Score:	524.50	Matches:	102
Percent Similarity:	89.17%	Conservative:	5
Best Local Similarity:	85.00%	Mismatches:	12
Query Match:	77.93%	Indels:	1
DB:	2	Gaps:	1

US-10-049-868A-2 (1-363) x A32456 (1-139)

QY 4	GTGCAGCTGCAGGAGTCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACT	63
Db 21	ValHisLeuLysGluSerGlyProValLeuValAlaProSerGlnSerLeuSerIleThr	40
QY 64	TGCACGTGCTCTGGGATTTCATTAAACAGATATGGTGTAACAGATATGGTTCGCCAGCCTCCA	123

Db 41 CysThrValSerGlyPheSerLeuThrAsnTyrGlyValHisTrpValArgGlnProPro 60

QY 124 GGAAAGGCTCTGGAGTGGGAGTAATATGGACTGGTGGGAAGCACAAATTATAATTCG 183

Db 61 GlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlyAsnThrAsnTyrAsnSer 80

QY 184 GCTCTCATGTCCAGACTGAGCATCAGCAAAAGACAACTCCAAGAGCCAAAGTTTCTTAAAA 243

Db 81 AlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeuLys 100

QY 244 ATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCTACT 303

Db 101 MetAsnSerLeuGlnIleAspAspThrAlaIleTyrTyrCysAlaLys---ArgLeuGlu 119

QY 304 ATGATTACGGCCTATGCTATGGACTACTGGGGCCCAAGGACCAAGTCAACCGTCTCCTCA 363

Db 120 ArgIlePheTyrTyrAlaMetAspTyrTrpGlyGlnGlyThrServalThrValSerSer 139

RESULT 10

S11108

Ig heavy chain V region (clone NQ5-78.2.6) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000

C;Accession: S11108

R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.

Nature 304, 320-324, 1983

A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone

A;Reference number: S07331; MUID:83271467; PMID:6877353

A;Accession: S11108

A;Molecule type: mRNA

A;Residues: 1-112 <NAT>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 1.41e-43 Length: 112

Score: 521.00 Matches: 101

Percent Similarity: 85.83% Conservative: 2

Best Local Similarity: 84.17% Mismatches: 9

Query Match: 77.41% Indels: 8

DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x S11108 (1-112)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60

Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuVal**ProSerGlnSerLeuSerIle 20

QY 61 ACTTGCACTGCTCTGGGATTTCATTAAACAGATATGGTGACACTGGTTCGCCAGCCT 120

Db 21 ThrCysThrValSerGly**SerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40

QY 121 CCAGGAAAGGCTCTGGAGTGGGAGTAATATGGACTGGTGGGAAGCACAAATTATAAT 180

Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60

QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAAGACAACTCCAAGAGCCAAAGTTTCTTA 240

Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPhe** 80

QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCAGAGATCGATCT 300

Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyr**CysAlaArgAspArgGlu 100

QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGCGCAAGGACCAAGTTCACCGTCTCC 360

Db 101 -----AspTyrTrpGly**GlyThrServalThrValSer 112

RESULT 11

S11103

Ig heavy chain V region (clone NQ5-61.1.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000

C;Accession: S11103

R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.

Nature 304, 320-324, 1983

A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone

A;Reference number: S07331; MUID:83271467; PMID:6877353

A;Accession: S11103

A;Molecule type: mRNA

A;Residues: 1-115 <NAT>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 3.51e-43 Length: 115

Score: 517.00 Matches: 101

Percent Similarity: 85.12% Conservative: 2

Best Local Similarity: 83.47% Mismatches: 10

Query Match: 76.82% Indels: 8

DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x S11103 (1-115)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60

Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20

QY 61 ACTTGCACTGCTCTGGGATTTCATTAAACAGATATGGTGACACTGGTTCGCCAGCCT 120

Db 21 ThrCysThrValSerGly**SerLeuThrSer**GlyValHisTrpValArgGlnPro 40

QY 121 CCAGGAAAGGCTCTGGAGTGGGAGTAATATGGACTGGTGGGAAGCACAAATTATAAT 180

Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60

QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAAGACAACTCCAAGAGCCAAAGTTTCTTA 240

Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSer**ValPheLeu 80

QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300

Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspArgGly 100

QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGCGCAAGGACCAAGTTCACCGTCTCC 360

Db 101 Ala-----TyrTrpGly**GlyThrLeuValThrValSer 112

QY 361 TCA 363

Db 113 Ala 113

RESULT 12

S11099

Ig heavy chain V region (clone NQ2-17.4.1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000

C;Accession: S11099

R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.

Nature 304, 320-324, 1983

A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone

A;Reference number: S07331; MUID:83271467; PMID:6877353

A;Accession: S11099

A;Molecule type: mRNA

A;Residues: 1-114 <NAT>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 5.54e-43 Length: 114

Score: 515.00 Matches: 100

Percent Similarity: 84.30% Conservative: 2

Best Local Similarity: 82.64% Mismatches: 11

Query Match: 76.52% Indels: 8

DB: 2 Gaps: 1


```
US-10-049-868A-2 (1-363) x S11099 (1-114)
QY      1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20

QY      61 ACTTGCACTGTCTCTGGGATTTTCATTAAACAGATATGGTGTFACACTGGGTTCCGCCAGCCT 120
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      21 ThrCysThrValSerGly***SerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40

QY      121 CCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGGAAGCACAAATTATAAT 180
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      41 ProGlyLysGlyLeuGluTrpLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60

QY      181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAAGAGCCAAAGTTTCTTA 240
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSer***ValPheLeu 80

QY      241 AAAATGAACAGTCTGCAGACTGATGACACAGCCCATGTACTACTGTGCCAGAGATCGATCT 300
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      81 LysMetAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAsp***Gly 100

QY      301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCCAAGGACCAACCGGTACCCGTCTCC 360
      |||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      101 Ala-----TyrTrpGlyGlnGlyThrLeu***Thr***Ser 112

QY      361 TCA 363
      |||:::
Db      113 Ala 113

RESULT 13
S42484
Ig heavy chain V region (4B1 VH) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
C;Accession: S42484
R;Gilbert, D.; Brard, F.; Margaritte, C.; Delpesch, A.; Tron, F.
submitted to the EMBL Data Library, March 1994
A;Description: An idiotype D23-bearing polyspecific, murine anti-DNA monoclonal antibody
A;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
A;Reference number: S42484
A;Accession: S42484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <GIL>
A;Cross-references: EMBL:Z30962; NID:g461325; PIDN:CAA83216.1; PID:g461326
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:      3.07e-42      Length:      116
Score:          507.50      Matches:      98
Percent Similarity: 85.25%      Conservative: 6
Best Local Similarity: 80.33%      Mismatches: 11
Query Match:    75.41%      Indels:      7
DB:             2          Gaps:      2

US-10-049-868A-2 (1-363) x S42484 (1-116)
QY      1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      1 GlnValGlnLeuGlnSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20

QY      61 ACTTGCACTGTCTCTGGGATTTTCATTAAACAGATATGGTGTFACACTGGGTTCCGCCAGCCT 120
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      21 ThrCysThrValSerGlyPheSerLeuThrSerTyrAlaIleSerTrpValArgGlnPro 40

QY      121 CCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGGAAGCACAAATTATAAT 180
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpThrGlyGlyThrAsnTyrAsn 60

QY      181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAAGAGCCAAAGTTTCTTA 240
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
```

```
Db      61 SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnIlePheLeu 80

QY      241 AAAATGAACAGTCTGCAGACTGATGACACAGCCCATGTACTACTGTGCCAGAGATCGATCT 300
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      81 LysLeuAsnSerLeuGlnThrAspAlaAlaArgTyrPheCysAlaArgAsp----- 98

QY      301 ACTATGATTACGGCCTATGCT---ATGGACTACTGGGGCCCAAGGACCAACCGGTACCCGTC 357
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      99 -----GlyTyrSerPhePheAspTyrTrpGlyGlnGlyThrThrLeuThrVal 114

QY      358 TCCTCA 363
      |||:::
Db      115 SerSer 116

RESULT 14
A49049
Ig heavy chain V region (anti-idiotypic) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
C;Accession: A49049
R;Armandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.
Eur. J. Immunol. 22, 2893-2899, 1992
A;Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR antigen
A;Reference number: A49049; MUID:93049629; PMID:1425914
A;Accession: A49049
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-122 <ARM>
A;Experimental source: BALB/c
A;Note: sequence extracted from NCBI backbone (NCBIN:118295, NCBIIP:118296)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.:      1.51e-41      Length:      122
Score:          500.50      Matches:      99
Percent Similarity: 86.78%      Conservative: 6
Best Local Similarity: 81.82%      Mismatches: 13
Query Match:    74.37%      Indels:      3
DB:             2          Gaps:      2

US-10-049-868A-2 (1-363) x A49049 (1-122)
QY      1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20

QY      61 ACTTGCACTGTCTCTGGGATTTTCATTAAACAGATATGGTGTFACACTGGGTTCCGCCAGCCT 120
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      21 ThrCysThrValSerGlyPheSerIleThrAspTyrValValSerTrpIleArgGlnPro 40

QY      121 CCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGGAAGCACAAATTATAAT 180
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpGlyGlyGlyAsnThrTyrTyrAsn 60

QY      181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAAGAGCCAAAGTTTCTTA 240
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      61 SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80

QY      241 AAAATGAACAGTCTGCAGACTGATGACACAGCCCATGTACTACTGTGCCAGAGATCGATCT 300
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      81 LysMetAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaLysHisAspGlu 100

QY      301 ACTATGATTACGGCCTATGCTATGGACTACTGGGAGTAATATGGACTGGTGGGAAGCACAAAGTCTCC 360
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      101 -----IleThrThrTyr---PheAspTyrTrpGlyGlnGlyThrThrLeuThrValSer 117

QY      361 TCA 363
      |||:::
Db      118 Ser 118

RESULT 15
```


S26322
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C;Accession: S26322
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26322
A;Molecule type: mRNA
A;Residues: 1-106 <STA>
A;Cross-references: EMBL:X59182
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-91/Domain: immunoglobulin homology <IMM>

Alignment Scores:			
Pred. No.:	1.7e-41	Length:	106
Score:	500.00	Matches:	97
Percent Similarity:	86.84%	Conservative:	2
Best Local Similarity:	85.09%	Mismatches:	7
Query Match:	74.29%	Indels:	8
DB:	2	Gaps:	1
US-10-049-868A-2 (1-363) x S26322 (1-106)			
QY	19	TCTGGACCTGGCGCTGGTGGCGCCCTCACAGAGCCTGTCCATCACTTGCACTGTCTCTGGG	78
Db	1	SerGlyProGlyLeuValAlaProSerGlnSerLeuSerIleThrCysThrValSerGly	20
QY	79	ATTTCAATAAACAGATATGGTGTACACTGGGTTCCGCCAGCCTCCAGGAAAGGGTCTGGAG	138
Db	21	PheSerLeuThrSerTyrGlyValHisTrpValArgGlnProProGlyLysGlyLeuGlu	40
QY	139	TGGCTGGGAGTAATATGGACTGGTGGAGCACAAATTATATTTCGGCTCTCATGTCCAGA	198
Db	41	TrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsnSerAlaLeuMetSerArg	60
QY	199	CTGAGCATCAGCAAGACAACTCCAAGAGCCAGTTTCTTAAAAATGAACAGTCTGCAG	258
Db	61	LeuSerIleSerLysAspAsnSerLysSerGlnValPheLeuLysMetAsnSerLeuGln	80
QY	259	ACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCTACTATGATTACGGCCTAT	318
Db	81	ThrAspAspThrAlaMetTyrTyrCysAlaArgGlu-----	92
QY	319	GCTATGGACTACTGGGCCCAAGGGACCAACCGGTCAACCGTCTCC	360
Db	93	AlaLeuArgLeuTrpGlyGlnGlyThrLeuValThrValSer	106

Search completed: October 13, 2004, 13:29:39
Job time : 23.6191 secs

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GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 13, 2004, 13:01:14 ; Search time 104.325 Seconds
(without alignments)
4004.053 Million cell updates/sec

Title: US-10-049-868A-2
Perfect score: 673
Sequence: 1 caggtgcagtcgaggatc.....ccacggtcaccgtctctca 363

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 3650362

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=UniProt_02 -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10049868@cgn_1_1_305@runat_13102004_132817_24791 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	506.5	75.3	482	Q91X92	Q91x92 mus musculu
2	490.5	72.9	121	Q99NG4	Q99ng4 mus musculu
3	487	72.4	144	HV43_MOUSE	P01819 mus musculu
4	442	65.7	115	HV44_MOUSE	P01820 mus musculu
5	436	64.8	116	HV45_MOUSE	P01821 mus musculu
6	401.5	59.7	135	HV02_XENLA	P20957 xenopus lae
7	389.5	57.9	465	Q6GMX6	Q6gm66 homo sapien
8	382	56.8	129	BAD00255	Bad00255 camelus d
9	376	55.9	119	Q9UL73	Q9ul73 homo sapien
10	373	55.4	121	HV3J_HUMAN	P01771 homo sapien
11	371.5	55.2	620	Q96EY0	Q96ey0 homo sapien
12	366	54.4	476	Q6GMX1	Q6gm61 homo sapien
13	364.5	54.2	477	Q6GMX7	Q6gm67 homo sapien
14	364.5	54.2	576	Q6P4I8	Q6p4i8 homo sapien
15	364.5	54.2	576	AAH63384	Aah63384 homo sapi
16	364	54.1	137	HV46_MOUSE	P01822 mus musculu

17	361.5	53.7	124	2	BAD00233	Bad00233 camelus d
18	358.5	53.3	478	2	Q72379	Q72379 homo sapien
19	356.5	53.0	573	2	Q8WJ38	Q8wu38 homo sapien
20	355	52.7	483	2	BAC85202	Bac85202 homo sapi
21	354	52.6	595	2	Q8WUX4	Q8wux4 homo sapien
22	354	52.6	597	2	Q6GMX5	Q6gm65 homo sapien
23	354	52.6	597	2	Q9BU10	Q9bul0 homo sapien
24	354	52.6	625	2	Q96AA6	Q96aa6 homo sapien
25	353.5	52.5	112	2	Q9HCC1	Q9hcc1 homo sapien
26	353	52.5	499	2	Q8N5K4	Q8n5k4 homo sapien
27	352	52.3	472	2	Q6N089	Q6n089 homo sapien
28	352	52.3	472	2	CAE45781	Cae45781 homo sapi
29	352	52.3	501	2	BAC85359	Bac85359 homo sapi
30	351	52.2	136	1	HV01_XENLA	P20956 xenopus lae
31	350	52.0	120	2	BAD00465	Bad00465 camelus d
32	350	52.0	128	2	BAD00406	Bad00406 camelus d
33	348.5	51.8	122	1	HV3G_HUMAN	P01768 homo sapien
34	348	51.7	597	2	Q9BQB8	Q9bqb8 homo sapien
35	347	51.6	479	2	BAC85434	Bac85434 homo sapi
36	346	51.4	470	2	BAC85387	Bac85387 homo sapi
37	345.5	51.3	118	2	Q811U5	Q81lu5 mus musculu
38	344.5	51.2	613	2	Q8WUK1	Q8wuk1 homo sapien
39	343	51.0	139	2	Q86SX2	Q86sx2 homo sapien
40	342.5	50.9	120	2	AAL35864	Aal35864 lama glam
41	341.5	50.7	136	2	Q6LBQ5	Q6lbq5 mus musculu
42	341.5	50.7	136	2	CAA34714	Caa34714 mus muscu
43	341	50.7	472	2	BAC85393	Bac85393 homo sapi
44	340	50.5	254	2	BAC86524	Bac86524 homo sapi
45	339.5	50.4	494	2	BAC85198	Bac85198 homo sapi

ALIGNMENTS

RESULT 1
Q91X92
ID Q91X92 PRELIMINARY; PRT; 482 AA.
AC Q91X92;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC011181; AAH11181.1; -.
DR PIR; F33932; F33932.
DR HSSP; P01820; 1A7N.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 482 AA; 51864 MW; 312E01F9C1BC7F3C CRC64;

Alignment Scores: 4.36e-48 Length: 482
Pred. No.: 506.50 Matches: 100
Score: 86.18% Conservative: 6
Best Local Similarity: 81.30% Mismatches: 10
Query Match: 75.26% Indels: 7
DB: 2 Gaps: 2

US-10-049-868A-2 (1-363) x Q91X92 (1-482)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCTGGCTGGTGGCGCCCTCAGAGAGCCTGTCCATC 60
Db GlnValGlnLeuLysGluSerGlyProAspLeuValAlaProSerGlnSerLeuSerIle 39
QY 61 ACTTGCACTGTCTCTGGGATTTCAATTAACAGATATGGTGACACTGGGTTGCCAGCCT 120
Db ThrCysThrValSerGlyPheAlaLeuThrSerTyrAlaIleSerTrpValArgGlnPro 59
QY 121 CCAGGAAAGGCTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGGAAGCACAAATTATAAT 180
Db ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpThrGlyValThrAsnTyrAsn 79
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACCTCCAAGACCAAGTTTCTTA 240
Db SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 99
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
Db LysMetAsnSerLeuGlnThrAsnAspThrAlaArgTyrTyrCysAlaArgAspSerAsn 119
QY 301 ACTATGATTACGGCCTAT-----GCTATGGACTACTGGGGCCCAAGGACCACGGTCACC 354
Db -----TyrGluGlyAlaMetAspTyrTrpGlyGlnGlyThrSerValThr 134
QY 355 GTCTCCTCA 363
Db ValSerSer 137

RESULT 2
Q99NG4 PRELIMINARY; PRT; 121 AA.
ID Q99NG4
AC Q99NG4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Single chain Fv (Fragment).
OS Mus musculus (Mouse).
OG plasmid PHEN1.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=98169018; PubMed=9510199;
RA Hawlisch H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L.,
RA Bautsch W., Kola A., Klos A., Koehl J.;
RT "Site-Directed C3a-Receptor Antibodies from Phage Display Libraries.";

RL J. Immunol. 160:2947-2958(1998).
DR EMBL; AJ222590; CAA10890.1; -.
DR PIR; F33932; F33932.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Plasmid.
FT NON_TER 1 1
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13255 MW; D293E4EBC8C59D5B CRC64;
Alignment Scores: 2.32e-46 Length: 121
Pred. No.: 490.50 Matches: 96
Score: 85.95% Conservative: 8
Best Local Similarity: 79.34% Mismatches: 16
Query Match: 72.88% Indels: 1
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x Q99NG4 (1-121)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCTGGCTGGTGGCGCCCTCAGAGAGCCTGTCCATC 60
Db GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGTCTCTGGGATTTCAATTAACAGATATGGTGACACTGGGTTGCCAGCCT 120
Db ThrCysThrValSerGlyPheProLeuThrSerHisGlyValSerTrpValArgGlnPro 40
QY 121 CCAGGAAAGGCTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGGAAGCACAAATTATAAT 180
Db ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpGlyAspGlyAsnThrLysTyrHis 60
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACCTCCAAGACCAAGTTTCTTA 240
Db SerAlaLeuIleSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
Db LysLeuAsnSerLeuGlnThrGluAspThrAlaThrTyrTyrCysAlaArg--HisTyr 99
QY 301 ACTATGATTACGGCCTATGTCTATGGACTACTGGGGCCCAAGGACCACGGTCACCGTCTCC 360
Db TyrLysTyrAlaAsnTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrValSer 119
QY 361 TCA 363
Db Ser 120

RESULT 3
HV43 MOUSE STANDARD; PRT; 144 AA.
ID HV43 MOUSE
AC P01819;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Ig heavy chain V region MOPC 141 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
RT of complete immunoglobulin heavy-chain genes."
RL Nature 286:676-683(1980).
CC -!- MISCELLANEOUS: The sequence shown is translated from a
CC differentiated gene isolated from a myeloma that secretes IgG2b.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

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DR EMBL; J00491; AAA38121.1; -.
DR PIR; A02094; G2MS14.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 144 Ig heavy chain V region MOPC 141.
FT DOMAIN 20 130 Ig-like.
FT NON TER 144
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Alignment Scores:
Pred. No.: 5.92e-46 Length: 144
Score: 487.00 Matches: 97
Percent Similarity: 81.25% Conservative: 7
Best Local Similarity: 75.78% Mismatches: 14
Query Match: 72.36% Indels: 10
DB: 1 Gaps: 2

US-10-049-868A-2 (1-363) x HV43_MOUSE (1-144)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCTGGTGGCGCCCTCAGAGCCTGTCCATC 60
Db 20 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 39
QY 61 ACTTGCACTGCTCTGGATTTCATTAAACAGATATGGTGACACGTGGTTCGCCAGCCT 120
Db 40 ThrCysThrValSerGlyPheSerLeuThrGlyTyrGlyValAsnTrpValArgGlnPro 59
QY 121 CCAGGAAGGGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCACAAATTATAAT 180
Db 60 ProGlyLysGlyLeuGluTrpLeuGlyThrIleTrpGlyAsnGlySerThrAspTyrAsn 79
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGCAACTCAAGAGCCAGTTTCTTAA 240
Db 80 SerThrLeuLysSerArgLeuThrIleThrLysAspAsnSerLysSerGlnValPheLeu 99
QY 241 AAATGAACAGTCTGCAGACTGATGACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
Db 100 LysMetAsnSerLeuGlnThrAspThrAlaArgTyrTyrCysAla-----Ser 116
QY 301 ACTATGATTACGGCCTAT-----GCTATGGACTACTGGGCCAA 339
Db 117 ValSerIleTyrTyrTyrGlyArgSerAspLysTyrPheThrLeuAspTyrTrpGlyGln 136
QY 340 GGGACACCGTCCACCGTCTCTCTCA 363
Db 137 GlyThrSerValThrValSerSer 144

RESULT 4
HV44_MOUSE
ID HV44_MOUSE STANDARD; PRT; 115 AA.
AC P01820;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig heavy chain V region PJ14 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
RT of complete immunoglobulin heavy-chain genes."
RL Nature 286:676-683(1980).
CC -! SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC -----

DR EMBL; V00767; CAA24148.1; -.
DR PIR; A02095; HVMS14.
DR PDB; 1A7N; X-ray; H=20-115.
DR PDB; 1A7O; X-ray; H=20-115.
DR PDB; 1A7P; X-ray; H=20-115.
DR PDB; 1A7R; X-ray; H=20-115.
DR PDB; 1G7H; X-ray; B=20-115.
DR PDB; 1G7I; X-ray; B=20-115.
DR PDB; 1G7J; X-ray; B=20-115.
DR PDB; 1G7M; X-ray; B=20-115.
DR PDB; 43C9; X-ray; B/D/F/H=19-115.
DR PDB; 43CA; X-ray; B/D/F/H=20-115.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 115 Ig heavy chain V region PJ14.
FT DOMAIN 20 >115 Ig-like.
FT STRAND 22 26
FT STRAND 30 30
FT STRAND 37 44
FT TURN 48 49
FT STRAND 52 58
FT TURN 60 61
FT STRAND 65 70
FT TURN 72 73
FT STRAND 76 78
FT TURN 80 82
FT HELIX 83 85
FT STRAND 86 91
FT HELIX 92 94
FT TURN 95 95
FT STRAND 96 101
FT HELIX 106 108
FT STRAND 110 115
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12447 MW; 7569DD4A4843D500 CRC64;

Alignment Scores:
Pred. No.: 7.13e-41 Length: 115
Score: 442.00 Matches: 85
Percent Similarity: 92.71% Conservative: 4
Best Local Similarity: 88.54% Mismatches: 7
Query Match: 65.68% Indels: 0
DB: 1 Gaps: 0

US-10-049-868A-2 (1-363) x HV44_MOUSE (1-115)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCTGGTGGCGCCCTCAGAGCCTGTCCATC 60
Db 20 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 39

```
QY      61  ACTTGCACTGTCTCTGGGATTTTCATTAAACAGATATGGTGTAACACTGGGTTCCGCCAGCCT 120
      |||||||
Db      40  ThrCysThrValSerGlyPheSerLeuThrGlyTyrGlyValAsnTrpValArgGlnPro 59
      |||||||
QY      121 CCAGGAAAGGGTCTGGAGTGGCTGGAGTAATATGGACTGGTGGGAAGCACAAATTATAAT 180
      |||||||
Db      60  ProGlyLysGlyLeuGluTrpLeuGlyMetIleTrpGlyAspGlySerThrAspTyrAsn 79
      |||||||
QY      181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCCAAGTTTCTTA 240
      |||||||
Db      80  SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 99
      |||||||
QY      241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCC 288
      |||||||
Db      100 LysMetAsnSerLeuGlnThrAspThrAlaArgTyrTyrCysAla 115
      |||||||

RESULT 5
HV45 MOUSE
ID HV45_MOUSE STANDARD; PRT; 116 AA.
AC P01821;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MC101 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82075900; PubMed=6273429;
RA Kataoka T., Nikaïdo T., Miyata T., Moriwaki K., Honjo T.;
RT "The nucleotide sequences of rearranged and germline immunoglobulin VH
RT genes of a mouse myeloma MC101 and evolution of VH genes in mouse.";
RL J. Biol. Chem. 257:277-285(1982).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
DR EMBL; J00502; AAA38515.1; -.
DR PIR; A02096; GIMS10.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 116 Ig heavy chain V region MC101.
FT DOMAIN 20 >116 Ig-like.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12593 MW; 8079A6EE7C552B3E CRC64;

Alignment Scores:
Pred. No.: 3.41e-40 Length: 116
Score: 436.00 Matches: 81
Percent Similarity: 92.78% Conservative: 9
Best Local Similarity: 83.51% Mismatches: 7
Query Match: 64.78% Indels: 0
DB: 1 Gaps: 0

US-10-049-868A-2 (1-363) x HV45_MOUSE (1-116)

QY      1  CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
      |||||||
Db      20  GlnValGlnLeuLysGlnSerGlyProGlyLeuValGlnProSerGlnSerLeuSerIle 39
      |||||||
```

```
QY      61  ACTTGCACTGTCTCTGGGATTTTCATTAAACAGATATGGTGTAACACTGGGTTCCGCCAGCCT 120
      |||||||
Db      40  ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnSer 59
      |||||||
QY      121 CCAGGAAAGGGTCTGGAGTGGCTGGAGTAATATGGACTGGTGGGAAGCACAAATTATAAT 180
      |||||||
Db      60  ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpSerGlyGlySerThrAspTyrAsn 79
      |||||||
QY      181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCCAAGTTTCTTA 240
      ::::|
Db      80  AlaAlaPheIleSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPhePhe 99
      ::::|
QY      241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCCAGA 291
      |||||||
Db      100 LysMetAsnSerLeuGlnSerAsnAspThrAlaIleTyrTyrCysAlaArg 116
      |||||||

RESULT 6
HV02 XENLA
ID HV02_XENLA STANDARD; PRT; 135 AA.
AC P20957;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region XIG14 precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88176921; PubMed=2451244;
RA Schwager J., Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
RT from cDNA sequence: implications for evolution of immunoglobulin
RT domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC -----
DR EMBL; J03632; AAA49791.1; -.
DR PIR; B31933; B31933.
DR HSSP; P01820; 1A7N.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 18
FT CHAIN 19 135 Ig heavy chain V region XIG14.
FT DOMAIN 20 128 Ig-like.
FT NON_TER 135 135
SQ SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;

Alignment Scores:
Pred. No.: 2.8e-36 Length: 135
Score: 401.50 Matches: 73
Percent Similarity: 77.97% Conservative: 19
Best Local Similarity: 61.86% Mismatches: 23
Query Match: 59.66% Indels: 3
DB: 1 Gaps: 1

US-10-049-868A-2 (1-363) x HV02_XENLA (1-135)
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```
QY 10 CTGCAGAGTCTGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCCTTGCACCT 69
Db 21 LeuGlnGluSerGlyProGlyThrValLysProSerGluSerLeuArgLeuThrCysThr 40
QY 70 GTCTCTGGGATTTCAATTAACAGATATGGTGTAACACTGGGTTCGCCAGCCTCCAGGAAAG 129
Db 41 ValSerGlyPheGluLeuSerSerTyrHisMetHisTrpIleArgGlnProProGlyLys 60
QY 130 GGTCTGGAGTGGCTGGAGTAATATGGACTGTGGGAAGCACAAATTATAATTTCGGCTCTC 189
Db 61 GlyLeuGluTrpIleGlyValIleAlaThrGlyGlySerThrAlaIleAlaAspSerLeu 80
QY 190 ATGTCCAGACTGAGCATCAGCAAGAACAACTCCAAGAGCCCAAGTTTCTTAAATAATGAAC 249
Db 81 LysAsnArgValThrIleThrLysAspAsnGlyLysLysGlnValTyrLeuGlnMetAsn 100
QY 250 AGTCTGCAGACTGATGACACAGCCATGTACTACTGTGTCAGAGATCGATCTACTATGATT 309
Db 101 GlyMetGluValLysAspThrAlaMetTyrTyrCysAlaArgGluTyrAla----- 117
QY 310 ACGGCCTATGCTATGACTACTGGGGCCCAAGGACCGGTCAACCGTCTCCTCA 363
Db 118 SerGlyTyrAsnPheAspTyrTrpGlyGlnGlyThrMetValThrValThrSer 135
RESULT 7
Q6GMX6
ID Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
Pfam; PF07654; C1-set; 3.
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DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Alignment Scores:
Pred. No.: 7.63e-35 Length: 465
Score: 389.50 Matches: 76
Percent Similarity: 76.86% Conservative: 17
Best Local Similarity: 62.81% Mismatches: 23
Query Match: 57.88% Indels: 5
DB: 2 Gaps: 1
```

US-10-049-868A-2 (1-363) x Q6GMX6 (1-465)

```
QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCTGGTGGCCCTCACAGAGCCTGTCCATC 60
Db 20 GlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeu 39
QY 61 ACTTGCACTCTCTCTGGGATTTCATTAAACAGATATGGTGTACACTGGGTTCGCCAGCCT 120
Db 40 ThrCysThrValSerGlyGlySerIleSerGlyTyrTyrTrpSerTrpIleArgGlnPro 59
QY 121 CCAGGAAAGCGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGGAAGCACAAATTATAAT 180
Db 60 AlaGlyLysGlyLeuGluTrpIleGlyArgIleTyrThrSerGlySerThrAsnTyrAsn 79
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAAAGACAACTCCAGAGCCAAAGTTTCTTA 240
Db 80 ProSerLeuLysSerArgValThrMetSerValAspThrSerLysAsnGlnPheSerLeu 99
QY 241 AAAATGAACAGTCTGCAGACTGTATGACACAGCCATGTACTACTGTCCAGAGATCGATCT 300
Db 100 LysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArgGlyArgPhe 119
QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGCAAGGACACACGGTCCCGTCTCC 360
Db 120 ThrTyr-----PheAspTyrTrpGlyGlnGlyThrLeuValThrValSer 134
QY 361 TCA 363
Db 135 Ser 135
```

RESULT 8

BAD00255
ID BAD00255 PRELIMINARY; PRT; 129 AA.

AC BAD00255;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.

OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Peripheral blood;

RA Honda T., Akahori Y., Kurosawa Y.;

RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and

RT gamma3 in vivo repertoires.";

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB091893; BAD00255.1; -.

DR NON_TER 1

FT NON_TER 129

SQ SEQUENCE 129 AA; 14117 MW; D9642F5A5BE3BEEE CRC64;

Alignment Scores:

Pred. No.: 4.49e-34 Length: 129
Score: 382.00 Matches: 75
Percent Similarity: 73.64% Conservative: 20
Best Local Similarity: 58.14% Mismatches: 26
Query Match: 56.76% Indels: 8
DB: 2 Gaps: 2

US-10-049-868A-2 (1-363) x BAD00255 (1-129)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCGCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 1 GlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGlnThrLeuThrLeu 20
QY 61 ACTTGCACTGTCTCTGGG-----ATTTCATTAAACAGATATGGTGATACACTGGGTTGCG 114
Db 21 ThrCysThrValSerGlyGlySerIleThrThrSerTyrTyrGlyTrpSerTrpIleArg 40
QY 115 CAGCCTCCAGGAAGGCTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCACAAAT 174
Db 41 GlnProProGlyLysGlyLeuGluTrpMetGlyAlaIleAlaTyrSerGlySerThrTyr 60
QY 175 TATAATTCGGCTCTCATGTCAGACTGAGCATCAGCAAGACAACTCCAGAGCCAAAGT 234
Db 61 TyrSerProSerLeuLysSerArgThrSerPheSerArgAspThrSerLysAsnGlnPhe 80
QY 235 TTCTTAAATAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGAT 294
Db 81 SerLeuGlnLeuSerSerValThrProGluAspThrAlaValTyrTyrCysAlaArgAsp 100
QY 295 CGA-----TCTACTATGATTACGGCCTATGCTATGGACTACTGGGCG 336
Db 101 SerProArgLeuArgValGlySerGluSerArgGlyValTyrSerMetAspTyrTrpGly 120
QY 337 CAAGGACCACGGTCCCGTCTCCTCA 363
Db 121 LysGlyThrLeuValThrIleSerSer 129

RESULT 9
Q9UL73

ID Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035041; AAD56277.1; -.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EA0BE CRC64;

Alignment Scores: 2.12e-33 Length: 119
Pred. No.: 376.00 Matches: 75
Score:

Percent Similarity: 74.38% Conservative: 15
Best Local Similarity: 61.98% Mismatches: 29
Query Match: 55.87% Indels: 2
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x Q9UL73 (1-119)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCGCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 1 GlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGlnThrLeuSerLeu 20
QY 61 ACTTGCACTGTCTCTGGGATTTCATTAAACAGATATGGTGATACACTGGGTTGCCAGCCT 120
Db 21 ThrCysThrValSerGlyGlySerIleCysSerTyrTyrTrpSerTrpIleArgGlnPro 40
QY 121 CCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGGAAGCACAAATTATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpIleGlyTyrIleTyrTyrSerGlySerThrAsnTyrThr 60
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAAGAGCCCAAGTTTCTTA 240
Db 61 ProSerLeuLysSerArgValThrIleSerValAspArgSerLysAsnGlnPheSerLeu 80
QY 241 AAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
Db 81 LysLeuThrSerLeuThrAlaAlaAspThrAlaValTyrPheCysAla-----ArgLeu 98
QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCCAAGGACCAACCGTCTCC 360
Db 99 SerAsnTrpGlyProTyrTyrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSer 118
QY 361 TCA 363
Db 119 Ser 119

RESULT 10
HV3J HUMAN

ID HV3J HUMAN STANDARD; PRT; 121 AA.
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region HIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=79124695; PubMed=420800;
RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT "Amino acid sequence of the VH region of human myeloma cryoimmunoglobulin IgG Hil.";
RL Biochemistry 18:553-560(1979).
CC -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02054; GIHJHL.
DR HSSP; P01772; 2PB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;


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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) .
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773; AAH73773.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Alignment Scores:
Pred. No.: 3.5e-32 Length: 476
Score: 366.00 Matches: 78
Percent Similarity: 71.32% Conservative: 14
Best Local Similarity: 60.47% Mismatches: 27
Query Match: 54.38% Indels: 10
DB: 2 Gaps: 3

US-10-049-868A-2 (1-363) x Q6GMX1 (1-476)
QY 1 CAGGTGCAGTCGACGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 20 GlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGlnThrLeuSerLeu 39
QY 61 ACTTGCACTGTCCTCTGGG-----ATTTCATTAACAGATATGGTGTFACACTGGTTCGC 114
Db 40 ThrCysThrValSerGlyGlySerIleSerSerGlyAspTyrTyrTrpSerTrpIleArg 59
QY 115 CAGCCTCCAGGAAGGGTCTGGAGTGGCTGGGAGTAGTAATATGGACTGGTGGGAAGCACAAAT 174
Db 60 GlnProProGlyLysGlyLeuGluTrpIleGlyTyrIleTyrSerGlySerThrTyr 79
QY 175 TATAATTCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACACTCCAAGAGCCAAAGTT 234
Db 80 TyrAsnProSerLeuLysSerArgValThrIleSerLeuAspThrSerLysAsnGlnPhe 99
QY 235 TTCTTAAAAATGACACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGAT 294
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Db 100 SerLeuLysMetAsnSerValThrAlaAlaAspThrAlaValTyrPheCysAlaAlaArgAla 119
QY 295 -----CGATCTACTATGATTACGGCCTATGCTATGGACTACTGGGC 336
Db 120 GlyValTrpGlySerPheArgSerTrpAlaIleAspGlyPhe-----AsnIleTrpGly 137
QY 337 CAAGGACCACGGTCACCGTCTCCTCA 363
Db 138 GlnGlyThrMetValThrValSerSer 146
RESULT 13
Q6GMX7
ID Q6GMX7 PRELIMINARY; PRT; 477 AA.
AC Q6GMX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) .
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073765; AAH73765.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; Cl-set; 2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;

Alignment Scores:
Pred. No.: 5.18e-32 Length: 477
Score: 364.50 Matches: 72
Percent Similarity: 73.55% Conservative: 17
Best Local Similarity: 59.50% Mismatches: 29
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Query Match: 54.16% Indels: 3
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x Q6GMX7 (1-477)

QY 1 CAGGTGCAGCTGTCAGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
|||||
Db 20 GlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGluThrLeuSerLeu 39

QY 61 ACTTGCACTGCTCTGGGATTTTCATTAAACAGATATGGTGTACACTGGGTTCGCCAGCCT 120
|||||
Db 40 ThrCysThrValSerGlyGlySerIleSerSerTyrtTyrTrpSerTrpIleArgGlnThr 59

QY 121 CCAGGAAAGGCTGGAGTGGCTGGGAGTAATATGGACTGGTGGGAAGCACAAATATAAT 180
|||||
Db 60 AlaGlyLysGlyLeuGluTrpIleGlyTyrIleSerHisSerGlySerThrThrTyraAsn 79

QY 181 TCGGCTCTCATGTCAGACTGAGCATCAGCAAGCAAACTCCAAGAGCCAAAGTTTCTTA 240
:::|
Db 80 ProSerLeuLysSerArgValThrLeuSerLeuAspThrSerLysAsnGlnPheSerLeu 99

QY 241 AAATGAACAGTTCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
:::|
Db 100 ArgLeuAsnSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaHisGlySerSer 119

QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCAAAGGACCAACCGTCAACCGTCTCC 360
:::|
Db 120 -----TrpAspPheAlaPheAspTyrTrpGlyGlnGlyThrLeuValThrValSer 136

QY 361 TCA 363
|||
Db 137 Ser 137

RESULT 14

Q6P4I8

ID Q6P4I8 PRELIMINARY; PRT; 576 AA.

AC Q6P4I8;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE IGHD protein.

GN Name=IGHD;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RN SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;

RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;

Alignment Scores:
Pred. No.: 5.32e-32 Length: 576
Score: 364.50 Matches: 76
Percent Similarity: 73.77% Conservative: 14
Best Local Similarity: 62.30% Mismatches: 29
Query Match: 54.16% Indels: 3
DB: 2 Gaps: 2

US-10-049-868A-2 (1-363) x Q6P4I8 (1-576)

QY 1 CAGGTGCAGCTGTCAGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
|||||
Db 27 GlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGlyThrLeuSerLeu 46

QY 61 ACTTGCACTGCTCTGGGATTTTCATTAAACAGATATGGT--GTACACTGGGTTCGCCAG 117
|||||
Db 47 ThrCysAlaValSerGlyGlySerIleSerSerSerAsnTrpTrpSerTrpValArgGln 66

QY 118 CCTCCAGGAAAGGCTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAAAGCACAAATTAT 177
|||||
Db 67 ProProGlyLysGlyLeuGluTrpIleGlyGluIleTyrHisSerGlySerThrAsnTyr 86

QY 178 AATTGGCTCTCATGTCCAGACTGAGCATCAGCAAAAGACAACCTCCAAGAGCCAAAGTTTC 237
|||:::|
Db 87 AsnProSerLeuLysSerArgValThrIleSerValAspLysSerLysAsnGlnPheSer 106

QY 238 TTAAAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGA 297
|||||
Db 107 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaSerLeuGly 126

QY 298 TCTACTATGATTACGGCCTATGCTATGGACTACTGGGGCCCAAGGACCAACCGTCAACCGT 357
|||
Db 127 Asp-----IleTyrTyrTyrGlyMetAspValTrpGlyGlnGlyThrThrValThrVal 144

QY 358 TCCTCA 363
|||||
Db 145 SerSer 146

RESULT 15

AAH63384

ID AAH63384 PRELIMINARY; PRT; 576 AA.

AC AAH63384;

DT 02-MAR-2004 (TrEMBLrel. 27, Created)

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RN SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -.
KW Hypothetical protein.
SQ SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;

Alignment Scores:

Pred. No.:	5.32e-32	Length:	576
Score:	364.50	Matches:	76
Percent Similarity:	73.77%	Conservative:	14
Best Local Similarity:	62.30%	Mismatches:	29
Query Match:	54.16%	Indels:	3
DB:	2	Gaps:	2

US-10-049-868A-2 (1-363) x AAH63384 (1-576)

QY	1	CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTCCATC	60
Db	27	GlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGlyThrLeuSerLeu	46
QY	61	ACTTGCACTGCTCTCTGGGATTTTCATTAAACAGATATGGT---GTACACTGGGTTCCGCCAG	117
Db	47	ThrCysAlaValSerGlyGlySerIleSerSerSerAsnTrpTrpSerTrpValArgGln	66
QY	118	CCTCCAGGAAGGGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGGAAGCACAAATTAT	177
Db	67	ProProGlyLysGlyLeuGluTrpIleGlyGluIleTyrHisSerGlySerThrAsnTyr	86
QY	178	AATTCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCAAGTTTTC	237
Db	87	AsnProSerLeuLysSerArgValThrIleSerValAspLysSerLysAsnGlnPheSer	106
QY	238	TTAAAAATGAACAGTCTGCAGACTGTATGACACAGCCATGTACTACTGTGCCAGAGATCGA	297
Db	107	LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaSerLeuGly	126
QY	298	TCTACTATGATTACGGCCTATGCTATGGACTACTGGGGCCCAAGGGACCGTCACCGTC	357
Db	127	Asp-----IleTyrTyrTyrGlyMetAspValTrpGlyGlnGlyThrThrValThrVal	144
QY	358	TCCTCA	363
Db	145	SerSer	146

Search completed: October 13, 2004, 13:28:08
Job time : 107.325 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 13, 2004, 13:00:14 ; Search time 82.9571 Seconds
(without alignments)
3139.425 Million cell updates/sec

Title: US-10-049-868A-2
Perfect score: 673
Sequence: 1 caggtgcagctgcaggagtc.....ccacggtcacgcgtctcctca 363

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 4004546

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2_1/USPTO_spool_p/US10049868/runat_13102004_132816_24785/app_query.fasta_1.1038
-DB=A Geneseq_23Sep04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10049868 @CGN_1_1_308 @runat_13102004_132816_24785 -NCFU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	557	82.8	113 2 AAR21268 Murine VH
2	555	82.5	115 8 ADF77174
3	553	82.2	125 6 ABR44627 Murine va
4	547	81.3	667 6 ABP97414
5	546	81.1	253 5 AAU72867
6	541.5	80.5	120 4 AAG63986
7	538	79.9	222 2 AAR32843
8	538	79.9	235 2 AAR32840
9	537	79.8	142 4 AAG66520
10	535	79.5	119 2 AAY49218

11	535	79.5	119	6	ADA14778	Adal4778	Peptide f
12	535	79.5	119	7	ADC35320	Adc35320	Anti-idio
13	534	79.3	123	2	AAW07438	Aaw07438	Anti-DNA
14	534	79.3	269	2	AAR32569	Aar32569	Fusion pr
15	532	79.0	476	4	AAB49243	Aab49243	Chimeric
16	531.5	79.0	140	2	AAW22538	Aaw22538	Murine an
17	531.5	79.0	140	5	AAE20201	Aae20201	Murine 44
18	531.5	79.0	140	8	ADJ31875	Adj31875	Murine 44
19	526	78.2	119	5	AAU72838	Aau72838	Anti-NKG2
20	525.5	78.1	242	2	AAR06483	Aar06483	18-2-3-/T
21	525.5	78.1	242	2	AAR43680	Aar43680	Single ch
22	525.5	78.1	242	2	AAR99650	Aar99650	Single ch
23	525.5	78.1	242	2	AAW02192	Aaw02192	18-2-3/TR
24	523	77.7	119	2	AAW42451	Aaw42451	Mouse ant
25	522.5	77.6	247	8	ADG28588	Adg28588	Paramyxov
26	522.5	77.6	287	6	ABR42057	Abr42057	Costimula
27	522.5	77.6	543	7	ADD12876	Add12876	CD28/mela
28	521.5	77.5	112	2	AAW31648	Aaw31648	Monoclona
29	521.5	77.5	239	2	AAW02191	Aaw02191	18-2-3/TR
30	521.5	77.5	241	2	AAR06482	Aar06482	18-2-3-/T
31	521	77.4	121	7	ADD25691	Add25691	Binding d
32	521	77.4	271	7	ADD25693	Add25693	Binding d
33	521	77.4	556	7	ADD25707	Add25707	Binding d
34	520.5	77.3	239	2	AAR43679	Aar43679	Single ch
35	520.5	77.3	239	2	AAR99649	Aar99649	Single ch
36	519	77.1	119	6	ABJ19263	Abj19263	Anti-huma
37	519	77.1	279	6	ABJ19275	Abj19275	Anti-huma
38	518.5	77.0	116	2	AAR40951	Aar40951	Mouse ger
39	518	77.0	119	2	AAR98478	Aar98478	MAB 2B6 h
40	517.5	76.9	116	4	AAU07513	Aau07513	Antibody
41	517.5	76.9	239	2	AAW09813	Aaw09813	VLLys-lin
42	517.5	76.9	239	2	AAW35561	Aaw35561	ECOR1-Hin
43	517.5	76.9	241	2	AAR21261	Aar21261	VHD1.3-Hu
44	517.5	76.9	267	2	AAR04841	Aar04841	Two linke
45	517.5	76.9	272	2	AAR21260	Aar21260	ScFV sequ

ALIGNMENTS

RESULT 1
AAR21268
ID AAR21268 standard; protein; 113 AA.
XX
AC AAR21268;
XX
DT 21-MAY-1992 (first entry)
XX
DE Murine VH group 2 chain E specific for phOx.
XX
KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
KW g3p; binding; adsorption; gene VIII; diverse repertoire;
KW specific binding pairs; replicable genetic display package.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Binding-site 31..35
FT Binding-site /label= CDR1
FT Binding-site 50..65
FT Binding-site /label= CDR2
FT Binding-site 98..102
FT Binding-site /label= CDR3
FT /note= " D/N-X-G-X-X motif "
XX
PN WO9201047-A.
XX
PD 23-JAN-1992.
XX
PF 10-JUL-1990; 90GB-00015198.
XX
PR 10-JUL-1990; 90GB-00015198.
PR 19-OCT-1990; 90GB-00022845.
PR 12-NOV-1990; 90GB-00024503.

PR 06-MAR-1991; 91GB-00004744.
PR 15-MAY-1991; 91GB-00010549.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA (MEDI-) MED RES COUNCIL.
XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD;
PI
XX WPI; 1992-056862/07.
DR
XX
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic display
PT package.
XX
PS Example 21; Fig 24; 209pp; English.
XX
CC The VH sequence is one of eight (AAR21264-71) found to be expressed from
CC a single chain Fv library from an immunised mouse. The library produces a
CC diverse repertoire of antibody fragments specific for 2-phenyl-5-
CC oxazolone (phOx). It was prep'd. using cDNA generated from mRNA from mice
CC immunised with phOx coupled to chicked serum albumin. The VH and VL kappa
CC sequences were separately amplified by PCR (see AAQ23474-84) and ligated
CC into fdCAT2 (see AAQ23463) for expression on the phage surface as fusions
CC with gene III. The resulting library of clones was diverse. Twenty three
CC hapten binding clones were sequenced revealing the eight different VH
CC genes (A-H) in a variety of pairings with seven different Vk genes (a-g)
CC (see AAR21264-92). Nearly all the VH genes belonged to gp 1, with only
CC one, "E", being of gp 2 (VHox1). Of the twenty three clones sequenced,
CC only one was of type "E". Most of the clones were Vk-d combinations. The
CC Kd of VH-B/Vk-d for phOx-GABA was 10 nM. Only two other combinations (of
CC eleven tested) were found to have higher values. This suggests that phage
CC bearing scFv fragments having weak affinities can be selected with
CC antigen, probably due to the avidity of the multiple antibody heads on
CC the phage. See also AAR21260-307, 309-311; AAR22450, 565-581
XX
SQ Sequence 113 AA;

Alignment Scores:

Pred. No.: 1.1e-47 Length: 113
Score: 557.00 Matches: 108
Percent Similarity: 89.26% Conservative: 0
Best Local Similarity: 89.26% Mismatches: 5
Query Match: 82.76% Indels: 8
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x AAR21268 (1-113)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 1 GlnValGlnLeuGlnGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGTCTCTGGGATTTTCATTAAACAGATATGGTGTAAGTGGTTCGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
QY 121 CCAGGAAAGGCTCTGGAGTGGCTGGAGTAATATGGACTGGTGAAGCACAAATTATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAAGACAACCTCCAAGAGSCCAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
Db 81 LysMetAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAspArgGly 100
QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCCAAGGACCACGGTCACCGTCTCC 360
Db 101 -----AspTyrTrpGlyGlnGlyThrThrValThrValSer 112
QY 361 TCA 363

Db 113 Ser 113
RESULT 2
ADF77174
ID ADF77174 standard; protein; 115 AA.
XX
AC ADF77174;
XX
DT 26-FEB-2004 (first entry)
XX
DE Anti-VAP-1 monoclonal antibody MoIG6 H chain.
XX complementarity determining region; CDR; mouse;
KW Vascular Adhesion Protein-1; VAP-1; antibody; heavy; light; chain;
KW chimeric; inflammatory disorder; rheumatoid arthritis;
KW inflammatory bowel disease; autoimmune disease; psoriasis;
KW immunoscintigraphic imaging.
XX
OS Mus sp.
XX
PN WO2003093319-A1.
XX
PD 13-NOV-2003.
XX
PF 28-APR-2003; 2003WO-FI000330.
XX
PR 29-APR-2002; 2002FI-00000807.
XX
PA (BIOT-) BIOTIE THERAPIES CORP.
PI Jalkanen S, Salmi M, Laukkanen M, Clark MR;
XX WPI; 2004-022642/02.
DR
XX
PT New chimeric anti-Vascular Adhesion Protein-1 monoclonal antibodies and
PT encoding nucleic acid molecules, useful for diagnosing and treating
PT chronic inflammatory disorders, e.g. rheumatoid arthritis or psoriasis.
XX
PS Disclosure; Fig 1; 56pp; English.
XX
CC This sequence represents a heavy chain variable region from a mouse anti-
CC Vascular Adhesion Protein-1 (VAP-1) antibody. This sequence is included
CC in the specification for comparison with the antibody of the invention.
CC The murine antibody sequences of the invention may be used in the
CC production of a chimeric mouse-human anti-VAP-1 antibody. The nucleic
CC acid molecules, polypeptides or antibodies are useful in treating VAP-1
CC mediated inflammatory disorders, such as rheumatoid arthritis,
CC inflammatory bowel disease, autoimmune diseases or psoriasis. The
CC chimeric VAP-1 antibody is further used for in vitro and in vivo
CC diagnostic applications, including in vivo immunoscintigraphic imaging of
CC inflammation sites. The chimeric MAB's of the invention have improved
CC kinetic properties compared to the corresponding murine antibodies.
XX
SQ Sequence 115 AA;
Alignment Scores:
Pred. No.: 1.76e-47 Length: 115
Score: 555.00 Matches: 106
Percent Similarity: 90.91% Conservative: 4
Best Local Similarity: 87.60% Mismatches: 5
Query Match: 82.47% Indels: 6
DB: 8 Gaps: 1
US-10-049-868A-2 (1-363) x ADF77174 (1-115)
QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGTCTCTGGGATTTTCATTAAACAGATATGGTGTAAGTGGTTCGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40

QY 121 CCAGGAAAGGTTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCACAAATTATAAT 180
|||||
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60

QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAGAGCAAGTTTCTTA 240
|||||
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80

QY 241 AAAATGAACAGTGCAGACTGATGACACAGCCATGTACTACTGTGCAGAGATCGATCT 300
|||||
Db 81 LysMetAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAsp----- 98

QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGCCCAAGGACCACGGFTCACCGTCTCC 360
:::|::|
Db 99 -----SerTyrSerPheAspTyrTrpGlyGlnGlyThrThrLeuThrValSer 114

QY 361 TCA 363
|||
Db 115 Ser 115

RESULT 3
ABR44627
ID ABR44627 standard; protein; 125 AA.
XX
AC ABR44627;
XX
DT 25-JUL-2003 (first entry)
XX
DE Murine variable heavy chain amino acid sequence MuVHIB.
XX
KW Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytostatic;
KW prostate specific membrane antigen; antipsoriatic; antiarthritic;
KW dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;
KW epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;
KW neoplastic disorder.
XX
OS Mus musculus.
OS Synthetic.
XX
PN WO2003024388-A2.
XX
PD 27-MAR-2003.
XX
PF 30-MAY-2002; 2002WO-US017204.
XX
PR 20-SEP-2001; 2001US-0324100P.
PR 08-MAR-2002; 2002US-0362612P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
XX Bander N;
XX
DR WPI; 2003-313319/30.
XX
PT Ablating/killing aberrant prostate specific membrane antigen-expressing
PT cells for treating skin disorders, by contacting the cell with an
PT antibody that binds to the extracellular domain of prostate specific
PT membrane antigen.
XX
PS Disclosure; Fig 12B; 225pp; English.
XX
CC The present invention describes a method (M1) for ablating or killing an
CC aberrant prostate specific membrane antigen (PSMA)-expressing cell (e.g.
CC an epidermal and a dermal cell). M1 comprises contacting the cell, or a
CC vascular endothelial cell proximate to the cell, with an antibody (or its
CC antigen-binding fragment), which binds specifically to the extracellular
CC domain of PSMA in an amount sufficient to ablate or kill the cell. The
CC antibodies have antipsoriatic, antiarthritic, dermatological, cytostatic,
CC antiinflammatory and antiallergic activities, and can be used in
CC vaccines. M1 is useful for treating a skin disorder in a subject, by
CC administering to the subject, an amount of an antibody which binds
CC specifically to the extracellular domain of PSMA (the subject is a

CC mammal, preferably human and is having, or at risk of, a skin disorder).
CC The skin disorder is a dermal or an epidermal disorder, and is selected
CC from psoriasis (preferably chronic stationary psoriasis, psoriasis
CC vulgaris, eruptive (gluttate) psoriasis, psoriatic erythroderma,
CC generalised pustular psoriasis (Von Zumbusch), annular pustular
CC psoriasis, and localised pustular psoriasis), psoriatic arthritis,
CC exfoliative dermatitis, pityriasis rubra pilaris, pityriasis rosacea,
CC parapsoriasis, pityriasis lichenoides, lichen planus, lichen nitidus,
CC ichthyosiform dermatosis, keratodermas, dermatosis, and prokeratosis,
CC preferably psoriasis. M1 is useful for treating a skin disorder such as
CC an inflammatory or neoplastic disorder of the epidermis or dermis,
CC preferably an epidermal precancerous or cancerous lesion. M1 is also
CC useful to treat or prevent disorders involving aberrant activity of PSMA-
CC expressing cell, e.g. kidney, liver or brain cell. ACC69816 to ACC69837
CC and ABR44613 to ABR44733 represent sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 125 AA;

Alignment Scores:
Pred. No.: 2.84e-47 Length: 125
Score: 553.00 Matches: 109
Percent Similarity: 89.60% Conservative: 3
Best Local Similarity: 87.20% Mismatches: 9
Query Match: 82.17% Indels: 4
DB: 6 Gaps: 2

US-10-049-868A-2 (1-363) x ABR44627 (1-125)

QY 1 CAGGTGCAGCTCAGGAGTCTGGACCTGGCTGGCGCCCTCAGAGAGCCTGTCCATC 60
|||
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20

QY 61 ACTTGCACGTCTCTCTGGGATTTTCATTAAACAGATATGGTGTACAC-----TGGTTTCGC 114
|||
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisValSerTrpValArg 40

QY 115 CAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCACAAAT 174
|||
Db 41 GlnProProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsn 60

QY 175 TATAATTCCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAAGAGCCAAAGTT 234
|||
Db 61 TyrAsnSerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnVal 80

QY 235 TTCTTAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGAT 294
|||
Db 81 PheLeuLysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAsp 100

QY 295 CGATCTACTATGATTACGGCC-----TATGCTATGGACTACTGGGGCCCAAGGACCACG 348
|||
Db 101 ArgGlyArgTyrTyrTyrSerGlyTyrTyrAlaMetAspTyrTrpGlyGlnGlyThrSer 120
:::

QY 349 GTCACCGTCTCCTCA 363
|||
Db 121 ValThrValSerSer 125

RESULT 4
ABP97414
ID ABP97414 standard; protein; 667 AA.
XX
AC ABP97414;
XX
DT 30-MAY-2003 (first entry)
XX
DE Anti-human seminal plasma protein ScFv/hCPA fusion protein.
XX
KW Single chain antibody; ScFv; anti-human seminal plasma protein;
KW monoclonal antibody E4B7; mouse; murine; human; carboxypeptidase A; hCPA;
KW fusion protein; antibody-directed enzyme prodrug therapy; ADEPT;
KW methotrexate-alpha-peptide prodrug; prostate cancer; cytostatic; gene;
KW ds.
XX

OS Mus musculus.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Protein 1..245
FT /label= E4B7-derived ScFv
FT /note= "Anti-human seminal plasma protein single chain
FT antibody derived from murine monoclonal antibody E4B7 VH
FT and VL regions; targets fusion protein to prostate cancer
FT cells"
FT
FT Region 1..122
FT /note= "Corresponds to monoclonal antibody E4B7 VH (heavy
FT chain variable region"
FT 123..137
FT /label= ScFv_linker
FT 138..245
FT /note= "Corresponds to monoclonal antibody E4B7 VL (light
FT chain variable region"
FT
FT Misc-difference 216
FT /note= "Encoded by GAC"
FT 245..251
FT /label= ScFv/hCPA_linker
FT 247
FT /note= "Encoded by AGC"
FT 253..667
FT /label= hCPA
FT /note= "Human carboxypeptidase A; activates methotrexate-
FT alpha-peptide prodrug"
XX
PN WO2002100431-A1.
XX
XX 19-DEC-2002.
XX
XX 08-JUN-2001; 2001WO-CN000924.
XX
XX 08-JUN-2001; 2001WO-CN000924.
XX (UYTA-) UNIV TANGDU HOSPITAL FORTH MILITARY MEDI.
PA (HAOX/) HAO X.
XX
PI Hao X;
XX
XX WPI; 2003-156924/15.
DR N-PSDB; ABZ75116.
DR
XX
PT Pharmaceutical kits for use in the treatment of prostate cancer, comprise
PT anti-human seminal plasma protein single-chain antibody/human
PT carboxypeptidase fusion protein and a prodrug of methotrexate-alpha-
PT peptides.
XX
PS Claim 3; Fig 4; 29pp; Chinese.
XX
XX The invention relates to a pharmaceutical kit for antibody-directed
CC enzyme prodrug therapy (ADEPT) to treat prostate cancer. The kit
CC comprises several respective containers for holding anti-human seminal
CC plasma protein single-chain antibody (ScFv)/human carboxypeptidase A
CC (hCPA) fusion protein (ABP97414), a prodrug of methotrexate-alpha-peptide
CC and a pharmaceutically-acceptable auxiliary for medication. The invention
CC also encompasses the anti-human seminal plasma protein ScFv/hCPA fusion
CC protein, and the nucleic acid encoding it (ABZ75116). This was
CC constructed by linking DNA encoding the ScFv (itself generated by linking
CC DNAs encoding the heavy and light chain variable regions (VH and VL) of
CC the murine anti-human seminal plasma protein monoclonal antibody E4B7) to
CC DNA encoding human carboxypeptidase A via a linker. The ScFv portion of
CC the fusion protein enables it to be specifically targeted to prostate
CC cancer cells, where the hCPA portion can then activate the prodrug which
CC in turn has cytostatic activity towards the cancer cells. The invention
CC permits the fusion protein to be easily produced in large quantities for
CC use in ADEPT for prostate cancer treatment. The present sequence
CC represents the ScFv/hCPA fusion protein of the invention
XX

SQ Sequence 667 AA;
Alignment Scores:
Pred. No.: 1.46e-46 Length: 667
Score: 547.00 Matches: 105
Percent Similarity: 91.74% Conservative: 6
Best Local Similarity: 86.78% Mismatches: 8
Query Match: 81.28% Indels: 2
DB: 6 Gaps: 1
US-10-049-868A-2 (1-363) x ABP97414 (1-667)
QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 2 GlnValGlnLeuGlnGluSerGlyProGlyLeuValAlaProSerGlnAsnLeuSerIle 21
QY 61 ACTTGCACTGTCTCTGGGATTTCATTAAACAGATATGGTGTACTGGTTCGCCAGCCT 120
Db 22 ThrCystThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 41
QY 121 CCAGGAAAGGGTCTGGAGTGGCTGGAGTAATATGGACTGGTGGAGCACAAATATAAT 180
Db 42 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpThrGlyArgSerThrThrTyrAsn 61
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAGAGCCCAAGTTTCTTA 240
Db 62 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerGluSerGlnValPheLeu 81
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
Db 82 LysMetAsnSerLeuGlnThrAspAspThrAlaIleTyrTyrCysGly-----ArgGly 99
QY 301 ACTATGATTACGGCCTATGCTATGGAAGTCTGGGGCCCAAGGACACGGTCACCGTCTCC 360
Db 100 GlyLeuIleThrSerPheAlaMetAspTyrTrpGlyGlnGlyThrThrValThrValSer 119
QY 361 TCA 363
Db 120 Ser 120
RESULT 5
AAU72867
ID AAU72867 standard; protein; 253 AA.
XX
AC AAU72867;
XX
DT 26-FEB-2002 (first entry)
XX
DE P5-9 single chain Fv.
XX
KW Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAPI0;
KW helminth; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;
KW 8G7C10; 6ESA7; 11B2D10x4-7; 8G7C10x4-7; 6ESA7x4-7; P4-2; P4-14;
KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
XX P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
OS Homo sapiens.
XX
XX WO200171005-A2.
XX
PD 27-SEP-2001.
XX
PF 26-MAR-2001; 2001WO-EP003414.
XX
PR 24-MAR-2000; 2000EP-00106467.
XX
PA (KUFE/) KUFER P.
XX
PI Kufer P, Riethmueller G, Lutterbuese R, Borschert K, Kischel R;

PI Mayer M, Hofmeister R;
XX WPI; 2002-055119/07.
DR N-PSDB; AAS97141.
XX
PT Multifunctional polypeptides comprising binding sites that specifically
PT recognize extracellular groups of the NKG2D receptor complex and domains
PT which function as receptors or ligands, useful for treating cancers and
PT infectious diseases.
XX
PS Example 7; Fig 16; 114pp; English.
XX
CC The invention relates to a multifunctional polypeptide comprising a
CC domain with a binding site that specifically recognises an extracellular
CC group of the NKG2D receptor complex and a second domain which functions
CC as a receptor or ligand. The polypeptide and its associated
CC polynucleotide are used for the preparation of a pharmaceutical
CC composition for the treatment of cancer, infections and/or autoimmune
CC conditions. The cancer may be a tumour of the head and neck, stomach,
CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
CC The infectious diseases can be caused by viruses, bacteria, fungi,
CC protozoa or helminths. The autoimmune diseases include multiple
CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
CC receptor and the polypeptides of the invention
XX
SQ Sequence 253 AA;

Alignment Scores:
Pred. No.: 1.6e-46 Length: 253
Score: 546.00 Matches: 108
Percent Similarity: 90.16% Conservative: 2
Best Local Similarity: 88.52% Mismatches: 8
Query Match: 81.13% Indels: 4
DB: 5 Gaps: 2

US-10-049-868A-2 (1-363) x AAU72867 (1-253)

QY 1 CAGGTGCAG---CTGCAGGAGTCTGGAGCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCC 57
Db 1 GluValGlnLeuLeuGluGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSer 20
QY 58 ATCACTTGCACCTGCTCTCTGGGATTTCATTAAACAGATATGGTGTACACTGGGTTGCCAG 117
Db 21 IleThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGln 40
QY 118 CCTCCAGGAAGGTCCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAAAGCACAAATTAT 177
Db 41 ProProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyr 60
QY 178 AATTCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCAAAGTTTTC 237
Db 61 AsnSerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPhe 80
QY 238 TTAATAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCAGAGATCGA 297
Db 81 LeuLysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspArg 100
QY 298 TCTACTATGATTACGGCCTATGCTATGGACTACTGGGGCCCAAGGGACCCGGTCACCGTC 357
Db 101 -----TyrTyrValGlyAlaMetAspTyrTrpGlyGlnGlyThrThrValThrVal 117
QY 358 TCCTCA 363
Db 118 SerSer 119
RESULT 6
AAG63986
ID AAG63986 standard; protein; 120 AA.

XX AAG63986;
AC
XX 26-NOV-2001 (first entry)
DT
XX Amino acid sequence of heavy chain variable region of antibody 2C4.
DE
XX Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;
KW allergy; asthma; anemia; eczema; lymphoma; systemic mastocytosis;
KW leukemia; eosinophil.
XX
OS Mus sp.
XX WO200166126-A1.
PN
XX 13-SEP-2001.
PD
XX 05-MAR-2001; 2001WO-US007193.
PF
XX 07-MAR-2000; 2000US-0187595P.
PR
XX (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (UYJO) UNIV JOHNS HOPKINS.
XX Abrahamson JA, Bochner B, Erickson-Miller CL, Kikly KK;
PI Schleimer R;
PI WPI; 2001-570749/64.
DR N-PSDB; AAH78183.
DR
XX Novel monoclonal antibody specific for human sialoadhesin factor-2 for
PT diagnosis, prevention, treatment of allergy, asthma, eczema or diseases
PT such as lymphoma, leukemia or systemic mastocytosis, in a mammal.
XX
PS Claim 17; Fig 1; 35pp; English.
XX
CC The present sequence represents the heavy chain variable region of murine
CC monoclonal antibody 2C4. This antibody binds to human sialoadhesin factor
CC -2 (SAF-2). The antibody is useful for treating or preventing allergic
CC rhinitis, allergies, asthma, anemia, eczema or diseases such as lymphoma,
CC leukemia or systemic mastocytosis in a mammal. It is also useful for
CC detecting the presence of a cell, especially eosinophil in a sample, by
CC detecting binding of the antibody to SAF-2. The antibody can be coupled
CC to toxins, antiproliferative drugs or radionuclides to kill cells in
CC areas of excessive SAF-2 expression
XX
SQ Sequence 120 AA;

Alignment Scores:

Pred. No.: 4.12e-46 Length: 120
Score: 541.50 Matches: 104
Percent Similarity: 91.74% Conservative: 7
Best Local Similarity: 85.95% Mismatches: 9
Query Match: 80.46% Indels: 1
DB: 4 Gaps: 1

US-10-049-868A-2 (1-363) x AAG63986 (1-120)

QY 1 CAGGTGCAGTGCAGGAGTCTGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGCTCTCTGGGATTTCATTAAACAGATATGGTGTACACTGGGTTGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrIleTyrGlyAlaHisTrpValArgGlnPro 40
QY 121 CCAGGAAAGGTCCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAAAGCACAAATTATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAGAGCCCAAGTTTCTTA 240
ID

Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80

QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCCATGTACTACTGTGCCAGAGATCGATCT 300
|||:::|||||
Db 81 LysIleAsnSerLeuGlnThrAspAspThrAlaLeuTyrTyrCysAlaArgAspGlySer 100
|||:::|||||
QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGCCCAAGGGACCAACGGTCACCGTCTCC 360
::: |||:::|||||
Db 101 SerProTyr---TyrTyrSerMetGluTyrTrpGlyGlnGlyThrSerValThrValSer 119
|||
QY 361 TCA 363
|||
Db 120 Ser 120

RESULT 7
AAR32843
ID AAR32843 standard; protein; 222 AA.
XX
AC AAR32843;
XX
DT 25-MAR-2003 (revised)
DT 19-JUN-1993 (first entry)
XX
DE VH NQ2/12.4-Vk NQ10/12.5 linked peptide sequences #2.
XX
KW Primer; human; immunoglobulin; Ig; variable region; VH; VL; Ck; JH;
KW lymphocyte; vector; soluble; antibody; phage; linker; back; VH3; nested;
KW in-cell PCR; cloning; polymorphic; TCR V; antiphenyloxazolone; hybridoma;
KW NQ2/12.4; NQ10/12.5.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .113
FT Peptide /label= VH_NQ2/12.4
FT 114. .115
FT /note= "Linker peptide"
FT 116. .222
FT /label= Vkappa_NQ2/12.4
XX
PN WO9303151-A1.
XX
PD 18-FEB-1993.
XX
PF 10-AUG-1992; 92WO-GB001483.
XX
PR 10-AUG-1991; 91GB-00017352.
PR 11-JUN-1992; 92GB-00012419.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Embleton MJ, Gorochev G, Jones PT, Winter GP;
XX
DR WPI; 1993-076508/09.
DR N-PSDB; AAQ37462.
XX
PT Treatment of cell populations, partic. hybridomas - to link together
XX copies of 2 or more non-contiguous DNA sequences to facilitate analysis.
XX
PS Disclosure; Fig 5; 72pp; English.
XX
CC The sequences given in AAR32840-43 show the mature heavy chain VH domains
CC and the Vk light chain genes of the antiphenyloxazolone hybridomas
CC NQ2/12.4 and NQ10/12.5 which have been linked via a linker peptide by in-
CC cell PCR. The cDNA encoding these peptides was synthesised using forward
CC primers annealing to the Ck gene and the JH segment, followed by assembly
CC with linker primers, VH back primers based on the VH3 leader sequence and
CC a forward Ck primer nested in respect to the primer used for cDNA. The
CC assembled product within the cells is then amplified with nested primers
CC annealing to the 5' end of the VH gene and the 3' end of the Jk segment.
CC In-cell PCR may be used to determine gene linkage analysis, particularly
CC for the cloning of gene combinations that are polymorphic within a
CC population of cells, such as the rearranged genes for Ig or TCR V

CC regions. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 222 AA;
Alignment Scores:
Pred. No.: 1.02e-45 Length: 222
Score: 538.00 Matches: 104
Percent Similarity: 87.60% Conservative: 2
Best Local Similarity: 85.95% Mismatches: 7
Query Match: 79.94% Indels: 8
DB: 2 Gaps: 1
US-10-049-868A-2 (1-363) x AAR32843 (1-222)
QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
|||:::|||||
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
|||:::|||||
QY 61 ACTTGCACTGTCTCTGGGATTTCAATAAACAGATATGGTGTAACACTGGTTCGCCAGCCT 120
|||:::|||||
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
|||:::|||||
QY 121 CCAGGAAAGGTCTGGAGTGGCTGGAGTAATATGGACTGGTGGAGACACAAATATAAT 180
|||:::|||||
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60
|||:::|||||
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAAGAGCCCAAGTTTCTTA 240
|||:::|||||
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
|||:::|||||
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCCATGTACTACTGTGCCAGAGATCGATCT 300
|||:::|||||
Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspArgGly 100
|||:::|||||
QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGCCCAAGGGACCAACGGTCTCC 360
|||:::|||||
Db 101 Ala-----TyrTrpGlyGlnGlyThrLeuValThrValSer 112
QY 361 TCA 363
::: |||
Db 113 Ala 113
RESULT 8
AAR32840
ID AAR32840 standard; protein; 235 AA.
XX
AC AAR32840;
XX
DT 25-MAR-2003 (revised)
DT 19-JUN-1993 (first entry)
XX
DE VH NQ2/12.4-Vk NQ10/12.5 linked peptide sequences.
XX
KW Primer; human; immunoglobulin; Ig; variable region; VH; VL; Ck; JH;
KW lymphocyte; vector; soluble; antibody; phage; linker; back; VH3; nested;
KW in-cell PCR; cloning; polymorphic; TCR V; antiphenyloxazolone; hybridoma;
KW NQ2/12.4; NQ10/12.5.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .113
FT Peptide /label= VH_NQ2/12.4
FT 114. .127
FT /note= "Linker peptide"
FT 128. .235
FT /label= Vkappa_NQ2/12.4
XX
PN WO9303151-A1.
XX
PD 18-FEB-1993.
XX
PF 10-AUG-1992; 92WO-GB001483.

XX 10-AUG-1991; 91GB-00017352.
PR 11-JUN-1992; 92GB-00012419.
XX (MEDI-) MEDICAL RES COUNCIL.
XX Embleton MJ, Gorochov G, Jones PT, Winter GP;
PI WPI; 1993-076508/09.
DR N-PSDB; AAQ37459.
XX Treatment of cell populations, partic. hybridomas - to link together
PT copies of 2 or more non-contiguous DNA sequences to facilitate analysis.
XX Disclosure; Fig 2; 72pp; English.
XX The sequences given in AAR32840-43 show the mature heavy chain VH domains
CC and the Vk light chain genes of the antiphenyloxazalone hybridomas
CC NQ2/12.4 and NQ10/12.5 which have been linked via a linker peptide by in-
CC cell PCR. The cDNA encoding these peptides was synthesised using forward
CC primers annealing to the Ck gene and the JH segment, followed by assembly
CC with linker primers, VH back primers based on the VH3 leader sequence and
CC a forward Ck primer nested in respect to the primer used for cDNA. The
CC assembled product within the cells is then amplified with nested primers
CC annealing to the 5' end of the VH gene and the 3' end of the Jk segment.
CC In-cell PCR may be used to determine gene linkage analysis, particularly
CC for the cloning of gene combinations that are polymorphic within a
CC population of cells, such as the rearranged genes for Ig or TCR V
CC regions. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 235 AA;
Alignment Scores:
Pred. No.: 1.02e-45 Length: 235
Score: 538.00 Matches: 104
Percent Similarity: 87.60% Conservative: 2
Best Local Similarity: 85.95% Mismatches: 7
Query Match: 79.94% Indels: 8
DB: 2 Gaps: 1
US-10-049-868A-2 (1-363) x AAR32840 (1-235)
QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGTCTCTGGGATTTTCATTAAACAGATATGGTGTACACTGGGTCGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
QY 121 CCAGGAAAGGCTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCAGCAAAATTATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCAAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGATCGATCT 300
Db 81 LysMetAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAspArgGly 100
QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGCGCCAAAGGACCACGGTCACCGTCTCC 360
Db 101 Ala-----TyrTrpGlyGlnGlyThrLeuValThrValSer 112
QY 361 TCA 363
Db 113 Ala 113
RESULT 9
AAG66520
ID AAG66520 standard; protein; 142 AA.

XX AAG66520;
AC
XX 22-OCT-2001 (first entry)
DT
DE Mouse antibody 26 heavy chain variable region.
XX Mouse; CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4;
KW immunosuppressive; immunomodulator; antiallergic; vaccine; antibody;
KW T cell; humanised antibody; autoimmune disorder; graft rejection;
KW allergy; antibody 26; heavy chain variable region; VH.
XX Mus musculus.
OS
XX WO200154732-A1.
PN
XX 02-AUG-2001.
PD
XX 26-JAN-2001; 2001WO-US002653.
PF
XX 27-JAN-2000; 2000US-0178473P.
PR
XX (GEMY) GENETICS INST INC.
PA
XX Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;
PI O'hara D, Hinton P, Tsurushita N;
PI
XX WPI; 2001-483195/52.
DR
DR N-PSDB; AAH76438.
XX
XX Novel antibody-toxic group conjugate comprising an antibody that
PT recognizes a molecule expressed only on activated T cells, useful for
PT modulating immune response for treating autoimmune disorder, allergic
PT response.
XX Example 7; Page 84; 123pp; English.
PS
XX The invention relates to an antibody-toxic group conjugate comprising an
CC antibody that specifically recognises a molecule expressed only on
CC activated T cells, and a toxic group. The T cell molecule is preferably
CC human cytotoxic T lymphocyte associated antigen 4 (CTLA4). The antibody
CC of the invention is a humanised anti-CTLA4 antibody comprising a sequence
CC of 128 or 142 amino acids fully defined in the specification. The
CC antibody-toxic group conjugate is useful for modulating the immune
CC response in a subject suffering from a disorder or condition such as
CC autoimmune disorder, immune response to a graft, allergic response or an
CC immune response to a therapeutic protein. The antibody is also useful for
CC research purposes, e.g., in staining and isolating CTLA4-bearing cells.
CC The antibody is also useful for T-cell typing, for isolating specific IL-
CC 2 receptor-bearing cells or fragments of the receptor, for vaccine
CC preparation, and for determining the effectiveness of an agent to down-
CC regulate CTLA4 activity. The present sequence is the heavy chain variable
CC region of mouse antibody 26. It was used in the construction of the
CC humanised anti-CTLA4 antibody of the invention
XX SQ Sequence 142 AA;
Alignment Scores:
Pred. No.: 1.21e-45 Length: 142
Score: 537.00 Matches: 104
Percent Similarity: 89.43% Conservative: 6
Best Local Similarity: 84.55% Mismatches: 11
Query Match: 79.79% Indels: 2
DB: 4 Gaps: 1
US-10-049-868A-2 (1-363) x AAG66520 (1-142)
QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 20 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 39
QY 61 ACTTGCACTGTCTCTGGGATTTTCATTAAACAGATATGGTGTACACTGGGTCGCCAGCCT 120
|||||

PT tumor in individual, by administering antibody containing light and heavy
PT chain variable region sequences contained in sequence of specified amino
PT acids.

XX
PS Example 2; Fig 3; 82pp; English.

XX The invention relates to the recurrence and/or development of a
CC ganglioside GD2-associated tumour, e.g. melanoma, in an individual which
CC is delayed by administration of an antibody comprising light and heavy
CC chain variable region sequences of the anti-idiotypic monoclonal antibody
CC 1A7. The antibody is used for delaying recurrence and/or development of
CC GD2-associated tumour, e.g. melanoma, neuroblastoma, glioma, sarcoma, or
CC small cell lung cancer, in individual, and for treating individual with
CC GD2-associated tumour. The present sequence is a unique peptide region
CC from an antibody sequence resembling the anti-idiotypic antibody 1A7 heavy
CC chain.

XX
SQ Sequence 119 AA;

Alignment Scores:
Pred. No.: 1.87e-45 Length: 119
Score: 535.00 Matches: 104
Percent Similarity: 88.43% Conservative: 3
Best Local Similarity: 85.95% Mismatches: 12
Query Match: 79.49% Indels: 2
DB: 6 Gaps: 1

US-10-049-868A-2 (1-363) x ADA14778 (1-119)

QY 1 CAGGTGCAGCTGCAGAGTCTGGACCTGGCCTGGTGGCGCCCTCACAGAGCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGTCTCTGGGATTTCATTAACAGATATGGTGACACTGGGTTCGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
QY 121 CCAGGAAGGGTCTGGAGTGGCTGGGAGTAATATCGACTGGTGGAGCAACAATTATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpGlyAspGlySerThrAsnTyrAsn 60
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAACAGCAACTCCAAGAGCCAAAGTTTCTTA 240
Db 61 SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACAGTCTGAGACTGATGACACAGCCATGTACTGTGCCAGAGATCGATCT 300
Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaArgTyrTyrCysAlaArgGlu***** 100
QY 301 ACTATGATTACGGCTATGCTATGGACTACTGGGCCCAAGGACCACGGTCACCGTCTCC 360
Db 101 *****TyrTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrValSer 118
QY 361 TCA 363
Db 119 Ser 119

RESULT 12
ADC35320
ID ADC35320 standard; protein; 119 AA.
XX
AC ADC35320;
XX
DT 18-DEC-2003 (first entry)
XX
DE Anti-idiotypic antibody VH region consensus sequence.

XX Mouse; monoclonal antibody; 1A7; anti-idiotypic antibody; ganglioside GD2;
KW cytostatic; melanoma; neuroblastoma; small cell lung cancer; tumour;
KW antibody; variable region; VH; VL; glioma; soft tissue sarcoma; vaccine.
XX
OS Synthetic.
OS Mus sp.

XX US2003114398-A1.
PN
XX 19-JUN-2003.
PD
XX 21-MAY-2002; 2002US-00153401.
PF
XX 17-JAN-1995; 95US-00372676.
PR 16-JAN-1996; 96US-00591196.
PR 15-APR-1999; 99US-00293533.
XX (CHAT/) CHATTERJEE M.
PA (FOON/) FOON K A.
PA (CHAT/) CHATTERJEE S K.
XX Chatterjee M, Foon KA, Chatterjee SK;
PI WPI; 2003-810913/76.
XX

PT Novel anti-idiotypic monoclonal antibody 1A7, that is capable of
PT recruiting a tumor-specific response against glycosphingolipid GD2,
PT useful for treating a GD2-associated disease e.g., melanoma, glioma, soft
PT tissue sarcoma.

XX Example 2; SEQ ID NO 16; 84pp; English.

CC The invention relates to a monoclonal antibody 1A7 (an anti-idiotypic
CC antibody eliciting an anti-GD2(ganglioside) response). Also included are
CC an antibody producing cell deposited under ATCC Accession No. HB-11786
CC (or its progeny), a polynucleotide comprising a sequence encoding a
CC polypeptide with immunological activity of 1A7 (where the polypeptide
CC comprises at least 5 consecutive amino acids from a variable region of
CC 1A7), an isolated polynucleotide comprising a region of at least 20
CC consecutive nucleotides that is capable of forming a stable duplex with a
CC polynucleotide encoding the light or heavy chain variable region of 1A7
CC under conditions where the region does not form a stable hybrid with a
CC polynucleotide consisting of a variable region encoding sequence
CC appearing as ADC35321 - ADC35370, a host cell comprising the
CC polynucleotide, a fusion polypeptide comprising 1A7, a humanised antibody
CC comprising 5 consecutive amino acids from the 1A7 variable regions and a
CC vaccine comprising the antibodies. The antibodies are useful for
CC eliciting an immune response in an individual, and for treating a GD2-
CC associated disease in an individual. The GD2-associated diseases is
CC chosen from melanoma, neuroblastoma, glioma, soft tissue sarcoma, and
CC small cell carcinoma. The individual has a clinically detectable tumour,
CC and the method is for palliating the GD2-associated disease. 1A7 is
CC preferably useful for treating a tumour that was previously detected in
CC the individual and has been treated and is clinically undetectable at the
CC time of the administering of 1A7, or for reducing the risk of recurrence
CC of a clinically detectable tumour. 1A7 and the humanised antibody are
CC useful for detecting the presence of an anti-GD2 antibody bound to a
CC tumour cell. The present sequence represents a consensus sequence for the
CC light or heavy chain variable region of monoclonal antibody 1A7.

XX Sequence 119 AA;

Alignment Scores:
Pred. No.: 1.87e-45 Length: 119
Score: 535.00 Matches: 104
Percent Similarity: 88.43% Conservative: 3
Best Local Similarity: 85.95% Mismatches: 12
Query Match: 79.49% Indels: 2
DB: 7 Gaps: 1

US-10-049-868A-2 (1-363) x ADC35320 (1-119)

QY 1 CAGGTGCAGCTGCAGAGTCTGGACCTGGCCTGGTGGCGCCCTCACAGAGCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGTCTCTGGGATTTCATTAACAGATATGGTGACACTGGGTTCGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40

QY 121 CCAGGAAGGCTCGAGTGGCTGGGAGTAATATGGACTGGTGGAGCACAATATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpGlyAspGlySerThrAsnTyrAsn 60
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACCTCCAAGAGCCAAAGTTTCTTA 240
Db 61 SerAlaLeuLysSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACACTCTGCAGACTGATGACACAGCCATGTACTACTGTGCAGAGATCGATCT 300
Db 81 LysMetAsnSerLeuGlnThrAspAspThrAlaArgTyrTyrCysAlaArgGlu***** 100
QY 301 ACTATGATTACGGCTATGCTATGGACTACTGGGGCCCAAGGACCAACCGTCAACGTCCTCC 360
Db 101 *****TyrTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrValSer 118
QY 361 TCA 363
Db 119 Ser 119
RESULT 13
AAW07438
ID AAW07438 standard; protein; 123 AA.
XX
AC AAW07438;
XX
DT 12-AUG-1997 (first entry)
XX
DE Anti-DNA antibody 11f8 group heavy chain variable region.
XX
KW Heavy chain; variable region; anti-DNA; monoclonal; antibody; 11f8 group;
KW hairpin; diagnosis; inflammatory glomerulonephritis;
KW systemic lupus erythematosus; screening; treatment; prevention; SLE;
KW disease; consensus; putative.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..30
FT /label= framework_I
FT Region 31..35
FT /label= CDR_I
FT Region 36..49
FT /label= framework_II
FT Region 50..66
FT /label= CDR_II
FT Region 67..98
FT /label= framework_III
FT Region 99..112
FT /label= CDR_III
FT Region 113..123
FT /label= J_region
XX
PN WO9636361-A1.
XX
XX
PD 21-NOV-1996.
XX
PF 16-MAY-1996; 96WO-US007113.
XX
PR 18-MAY-1995; 95US-00443540.
XX
PA (UNMI) UNIV MICHIGAN.
XX
PI Glick GD, Swanson PC;
XX
DR WPI; 1997-011854/01.
XX
PT Anti-DNA antibody which specifically binds DNA hairpin - useful to
PT develop prods. for diagnosis and treatment of disorders, e.g.
PT glomerulonephritis or systemic lupus erythematosus.
XX
PS Example; Fig 9; 102pp; English.

XX The present sequence is the heavy chain variable region of the group 11f8
CC putative consensus anti-DNA monoclonal antibody (MAB), which has a high
CC affinity for single stranded DNA, low or no affinity for double stranded
CC DNA and specifically binds a DNA hairpin. The MAB can be used to diagnose
CC disorders associated with the pathological complexation of DNA, e.g.
CC inflammatory glomerulonephritis and systemic lupus erythematosus. It can
CC also be used to generate reagents to screen for pharmaceutical agents,
CC and treat and/or prevent an above disorder. The sequence was derived by
CC aligning homologous anti-DNA MAB, whose sequences have been published, as
CC well as several MAB of other specificities obtained from a database
CC search
XX
SQ Sequence 123 AA;
Alignment Scores:
Pred. No.: 2.38e-45 Length: 123
Score: 534.00 Matches: 107
Percent Similarity: 88.62% Conservative: 2
Best Local Similarity: 86.99% Mismatches: 12
Query Match: 79.35% Indels: 2
DB: 2 Gaps: 2
US-10-049-868A-2 (1-363) x AAW07438 (1-123)
QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCTGGCGCCCTACAGAGCCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGTCTCTGGGATTTCAATAACAGATATGGTGTAACAGTTCGCCAGCCT 120
Db 21 ThrCystThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40
QY 121 CCAGGAAGGCTCTGGAGTGGCTGGAGTAATATGG---ACTGGTGGAAAGCACAAATTAT 177
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpProAlaGlyGlySerThrAsnTyr 60
QY 178 AATTCCGCTCTCATGTCCAGACTGACATCAGCAAGACAACCTCCAAGAGCCAAAGTTTC 237
Db 61 AsnSerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPhe 80
QY 238 TTAATAATGAACAGTCTGCAGACTCATGACACAGCCATGTACTACTGTGCCAGATCGA 297
Db 81 LeuLysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgHisLeu 100
QY 298 TCT---ACTATGATTACGGCCTATGCTATGGACTACTGGGCGCCAAAGGACCGTCACC 354
Db 101 ProTyrGlyAsnTyrGlyTyrTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThr 120
QY 355 GTCTCCTCA 363
Db 121 ValSerSer 123
RESULT 14
AAR32569
ID AAR32569 standard; protein; 269 AA.
XX
AC AAR32569;
XX
DT 25-MAR-2003 (revised)
DT 08-JUN-1993 (first entry)
XX
DE Fusion protein encoded by Ox VH-hinge-VL insert.
XX
KW Spacer peptide; secretable; single chain; antibody; recombinant; scAb;
KW rDNA; linker; Bos taurus.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..22
FT /note= "SS"
FT Region 23..135

FT /note= "VH"
FT 136..163
FT /note= "CBHI hinge"
FT 164..277
FT /note= "VL"
XX
PN FI9103434-A.
XX
PD 17-JAN-1992.
XX
XX
PF 16-JUL-1991; 91FI-00913434.
XX
XX 16-JUL-1990; 90US-00552751.
XX
PA (TERE-) TECH RES CENT FINLA.
XX
DR WPI; 1992-134225/17.
DR N-PSDB; AAQ36982.
XX
PT Sepd. recombinant fusion proteins.
XX
PS Example; Fig 4; 56pp; English.
XX
CC The sequence is that of the fusion protein encoded by the Ox VH-CBHI
CC hinge-VL insert which was used as part of a method for cloning
CC secretable, biologically active single chain antibodies (scAbs) and other
CC secretable fusion proteins having at least 2 distinct functional proteins
CC or domains. NOTE: This patent has been indexed using data derived from
CC patent WO9302198-A. (First Major Country Equivalent). (Updated on 25-MAR-
CC 2003 to correct PF field.)
XX
SQ Sequence 269 AA;

Alignment Scores:
Pred. No.: 2.65e-45 Length: 269
Score: 534.00 Matches: 103
Percent Similarity: 86.78% Conservative: 2
Best Local Similarity: 85.12% Mismatches: 8
Query Match: 79.35% Indels: 8
DB: 2 Gaps: 1

US-10-049-868A-2 (1-363) x AAR32569 (1-269)

QY 1 CAGGTGCAGCTGCAGAGTCTGGAGTCTGGACCTGGCTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 23 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 42
QY 61 ACTTGCACTGTCTCTGGGATTTTCATTAAACAGATATGGTGACACTGGGTTCGCCAGCCT 120
Db 43 ThrCysThrAlaSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 62
QY 121 CCAGGAAAGGTCCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCACAAATTATAAT 180
Db 63 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 82
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCAGTTTCTTA 240
Db 83 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 102
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGATCGATCT 300
Db 103 LysMetAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAspArgGly 122
QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCCAAGGGACCACGGTCACCGTCTCC 360
Db 123 Ala-----TyrTrpGlyGlnGlyThrLeuValThrValSer 134
QY 361 TCA 363
Db 135 Ala 135
RESULT 15
AAB49243

ID AAB49243 standard; protein; 476 AA.
XX
AC AAB49243;
XX
DT 15-MAR-2001 (first entry)
XX
DE Chimeric 4H6 anti-DR4 antibody heavy chain protein.
XX
KW Anti-Death receptor 4; DR4; antibody; apoptosis; cancer; arthritis;
KW autoimmune.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2000073349-A1.
XX
PD 07-DEC-2000.
XX
PF 25-MAY-2000; 2000WO-US014599.
XX
PR 28-MAY-1999; 99US-00322875.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Chuntharapai A, Dodge KH, Kim KJ;
XX
DR WPI; 2001-041145/05.
XX
PT Novel anti-death receptor 4 antibodies useful for treating cancer and
PT immune related disorders such as rheumatoid arthritis, sjogren's
PT syndrome, Grave's disease and diabetes mellitus.
XX
PS Claim 16; Fig 18; 126pp; English.
XX
CC The present invention relates to an anti-Death receptor 4 (DR4) antibody.
CC The antibodies of the invention are useful for inducing apoptosis in
CC mammalian cancer cells such as colon cancer cells and for treating an
CC immune-related disease in a mammal such as arthritis and autoimmune
CC disease
XX
SQ Sequence 476 AA;

Alignment Scores:

Pred. No.: 4.58e-45 Length: 476
Score: 532.00 Matches: 102
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 80.95% Mismatches: 7
Query Match: 79.05% Indels: 6
DB: 4 Gaps: 1

US-10-049-868A-2 (1-363) x AAB49243 (1-476)

QY 4 GTGCAGCTGCAGAGTCTGGACCTGGCTGGCGCCCTCACAGAGCCTGTCCATCACT 63
Db 21 ValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIleThr 40
QY 64 TGCACCTGTCTCTGGGATTTTCATTAAACAGATATGGTGACACTGGGTTCGCCAGCTCCA 123
Db 41 CysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnProPro 60
QY 124 GGAAGGTCCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCACAAATTATAATTCG 183
Db 61 GlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaValGlySerThrAsnTyrAsnSer 80
QY 184 GCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCCAAGTTTCTTAAAA 243
Db 81 AlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeuLys 100
QY 244 ATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGAT----- 294
Db 101 MetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgGlyGluPhe 120
QY 295 -----CGATCTACTATGATTACGGCCTATGCTATGGACTACTGGGGCCAAGGGACC 345

```
Db      121 AspTyrTyrGlySerSerLeuLeuSerTyrHisSerMetAsnPheTrpGlyGlnGlyThr 140
Qy      346 ACGGTCACCGTCTCCTCA 363
Db      141 SerValThrValSerSer 146
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	* Query			Description
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1	557	82.8	113	16	US-10-803-622-218	Sequence 218, App
2	557	82.8	113	16	US-10-803-653-218	Sequence 218, App
3	546	81.1	253	15	US-10-239-656-63	Sequence 63, Appl
4	537	79.8	142	9	US-09-772-103-4	Sequence 4, Appli
5	535	79.5	119	14	US-10-153-401-16	Sequence 16, Appl
6	532	79.0	476	16	US-10-660-128-12	Sequence 12, Appl
7	531.5	79.0	140	8	US-08-973-518-4	Sequence 4, Appli
8	531.5	79.0	140	9	US-09-007-093-4	Sequence 4, Appli
9	531.5	79.0	140	14	US-10-428-754-4	Sequence 4, Appli
10	531	78.9	119	14	US-10-232-187-2	Sequence 2, Appli
11	526	78.2	119	15	US-10-239-656-23	Sequence 23, Appl
12	523	77.7	119	14	US-10-144-644-15	Sequence 15, Appl
13	523	77.7	119	16	US-10-740-740-15	Sequence 15, Appl
14	521.5	77.5	112	9	US-09-824-286-3	Sequence 3, Appli
15	521	77.4	121	14	US-10-207-655-252	Sequence 252, App
16	521	77.4	271	14	US-10-207-655-254	Sequence 254, App
17	521	77.4	556	14	US-10-207-655-268	Sequence 268, App
18	517.5	76.9	116	14	US-10-169-351-108	Sequence 108, App
19	517.5	76.9	241	16	US-10-803-622-187	Sequence 187, App
20	517.5	76.9	241	16	US-10-803-653-187	Sequence 187, App
21	517.5	76.9	272	16	US-10-803-622-183	Sequence 183, App
22	517.5	76.9	272	16	US-10-803-653-183	Sequence 183, App
23	515.5	76.6	120	14	US-10-194-975-112	Sequence 112, App
24	514.5	76.4	116	14	US-10-194-975-100	Sequence 100, App
25	510.5	75.9	135	16	US-10-351-748-31	Sequence 31, Appl
26	510.5	75.9	135	17	US-10-351-748-31	Sequence 31, Appl
27	508.5	75.6	333	14	US-10-059-261-61	Sequence 61, Appl
28	505.5	75.1	139	8	US-08-779-784-37	Sequence 37, Appl
29	505.5	75.1	241	15	US-10-353-721-13	Sequence 13, Appl
30	503	74.7	249	9	US-09-730-374-3	Sequence 3, Appli
31	503	74.7	249	16	US-10-704-206-3	Sequence 3, Appli
32	502	74.6	121	11	US-09-842-776A-52	Sequence 52, Appl
33	501.5	74.5	116	15	US-10-435-299-4	Sequence 4, Appli
34	501.5	74.5	118	14	US-10-056-052-16	Sequence 16, Appl
35	500	74.3	121	14	US-10-056-052-12	Sequence 12, Appl
36	494.5	73.5	119	13	US-10-140-555-2	Sequence 2, Appli
37	494.5	73.5	139	9	US-09-881-823-4	Sequence 4, Appli
38	493.5	73.3	120	16	US-10-697-399-5	Sequence 5, Appli
39	491.5	73.0	135	14	US-10-010-729-68	Sequence 68, Appl
40	490.5	72.9	116	16	US-10-682-845-53	Sequence 53, Appl
41	490.5	72.9	492	16	US-10-682-845-59	Sequence 59, Appl
42	490.5	72.9	492	16	US-10-682-845-61	Sequence 61, Appl
43	490.5	72.9	492	16	US-10-682-845-63	Sequence 63, Appl
44	490.5	72.9	492	16	US-10-682-845-65	Sequence 65, Appl
45	490.5	72.9	492	16	US-10-682-845-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-10-803-622-218
; Sequence 218, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,622

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; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 218
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-218
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Alignment Scores:
Pred. No.:          2.05e-48          Length:          113
Score:              557.00           Matches:         108
Percent Similarity: 89.26%           Conservative:    0
Best Local Similarity: 89.26%        Mismatches:      5
Query Match:        82.76%           Indels:          8
DB:                 16               Gaps:           1
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US-10-049-868A-2 (1-363) x US-10-803-622-218 (1-113)

QY      1  CAGGTGCAGCTGCAGGAGTCTGGACCTGGCGCTGGCGCCCTCACAGAGCCTGTCCATC 60
Db      1  GlnValGlnLeuGlnGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20

QY      61  ACTTGCACTGTCTCTGGGATTTCATTAAACAGATATGGTGTACACTGGGTTGCCAGCCT 120
Db      21  ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40

QY      121  CCAGGAAAGGCTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCACAATAATTATAAT 180
Db      41  ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60

QY      181  TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCCAAGTTTCTTA 240
Db      61  SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80

QY      241  AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTGTGCCAGAGATCGATCT 300
Db      81  LysMetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspArgGly 100

QY      301  ACTATGATTACGGCCTATGCTATGGACTACTGGGCGCCAAAGGACCACGGFTCACCCTCTCC 360
Db      101  -----AspTyrTrpGlyGlnGlyThrThrValThrValSer 112

QY      361  TCA 363
Db      113  Ser 113

RESULT 2
US-10-803-653-218
; Sequence 218, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
```

```
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,653
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 218
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-218

Alignment Scores:
Pred. No.:          2.05e-48          Length:          113
Score:              557.00           Matches:         108
Percent Similarity: 89.26%           Conservative:    0
Best Local Similarity: 89.26%        Mismatches:      5
Query Match:        82.76%           Indels:          8
DB:                 16               Gaps:           1

US-10-049-868A-2 (1-363) x US-10-803-653-218 (1-113)

QY      1  CAGGTGCAGCTGCAGGAGTCTGGACCTGGCGCTGGCGCCCTCACAGAGCCTGTCCATC 60
Db      1  GlnValGlnLeuGlnGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20

QY      61  ACTTGCACTGTCTCTGGGATTTCATTAAACAGATATGGTGTACACTGGGTTGCCAGCCT 120
Db      21  ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 40

QY      121  CCAGGAAAGGCTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCACAATAATTATAAT 180
Db      41  ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60

QY      181  TCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACTCCAAGAGCCCAAGTTTCTTA 240
Db      61  SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80

QY      241  AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTGTGCCAGAGATCGATCT 300
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Db 81 LysMetAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAspArgGly 100
301 ACTATGATTACGGCCTATGCTATGGACTACTGGGCGCCAAAGGACCCACGGTCACCGTCTCTCC 360
Db 101 -----AspTyrTrpGlyGlnGlyThrThrValThrValSer 112
QY 361 TCA 363
Db 113 Ser 113
RESULT 3
US-10-239-656-63
; Sequence 63, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTTERBUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOFMEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; TITLE OF INVENTION: TO AN EPIOTOPE OF THE NKG2D RECEPTOR COMPLEX
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic P5-3 single
; OTHER INFORMATION: chain Fv
US-10-239-656-63

Alignment Scores:
Pred. No.: 3,01e-47 Length: 253
Score: 546.00 Matches: 108
Percent Similarity: 90.16% Conservative: 2
Best Local Similarity: 88.52% Mismatches: 8
Query Match: 81.13% Indels: 4
DB: 15 Gaps: 2
US-10-049-868A-2 (1-363) x US-10-239-656-63 (1-253)
QY 1 CAGGTGCAG---CTGCAGGAGTCTGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCC 57
Db 1 GluValGlnLeuLeuGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSer 20
QY 58 ATCACTTGCACGTCTCTGGGATTTTCATTAAACAGATATGTTGTACACTGGGTTCCGCCAG 117
Db 21 IleThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGln 40
QY 118 CCTCCAGGAAGGGTCTGGAGTGGCTGGGAGTAAATATGGACTGGTGGAAAGCACAAATTAT 177
Db 41 ProProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyr 60
QY 178 AATTCGGCTCTCATGTCCAGACTGAGCATCAGCAAGACAACCTCAAGAGCCCAAGTTTTC 237
Db 61 AsnSerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPhe 80
QY 238 TTAATAATGAACAGTCTGCAGACTGATGACACAGCCCATGTACTACTGTGCCAGAGATCGA 297
Db 81 LeuLysMetAsnSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAspArg 100

QY 298 TCTACTATGATTACGGCCTATGCTATGGACTACTGGGCGCCAAAGGACCCACGGTCACCGTC 357
Db 101 -----TyrTyrValGlyAlaMetAspTyrTrpGlyGlnGlyThrThrValThrVal 117
QY 358 TCCTCA 363
Db 118 SerSer 119
RESULT 4
US-09-772-103-4
; Sequence 4, Application US/09772103
; Publication No. US20020039581A1
; GENERAL INFORMATION:
; APPLICANT: Carreno, Beatriz M.
; APPLICANT: Wood, Clive
; APPLICANT: Turner, Katherine
; APPLICANT: Collins, Mary
; APPLICANT: Gray, Gary S.
; APPLICANT: Morris, Donna
; APPLICANT: O'Hara, Denise
; APPLICANT: Hinton, Paul
; APPLICANT: Tsurushita, Naoya
; TITLE OF INVENTION: ANTIBODIES AGAINST CTLA4 AND USES THEREFOR
; FILE REFERENCE: GNN-009CP
; CURRENT APPLICATION NUMBER: US/09/772,103
; CURRENT FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/178,473
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-772-103-4
Alignment Scores:
Pred. No.: 2.36e-46 Length: 142
Score: 537.00 Matches: 104
Percent Similarity: 89.43% Conservative: 6
Best Local Similarity: 84.55% Mismatches: 11
Query Match: 79.79% Indels: 2
DB: 9 Gaps: 1
US-10-049-868A-2 (1-363) x US-09-772-103-4 (1-142)
QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 20 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 39
QY 61 ACTTGCACTGTCTCTGGGATTTTCATTAAACAGATATGGTGTACACTGGGTTCCGCCGCCT 120
Db 40 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValTyrTrpValArgGlnPro 59
QY 121 CCAGGAAAGGCTCTGGAGTGGCTGGGAGTAAATATGGACTGGTGGAAAGCACAAATTATAAT 180
Db 60 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlyThrThrAsnTyrAsn 79
QY 181 TCGCTCTCATGTCCAGACTGAGCATCAGCAAAAGACAACCTCAAGAGCCCAAGTTTCTTA 240
Db 80 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 99
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCCATGTACTACTGTGCCAGA-----GAT 294
Db 100 LysMetSerSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgGlyProPro 119
QY 295 CGATCTACTATGATTACGGCCTATGCTATGGACTACTGGGCGCCAAAGGACCCACGGTCACC 354
Db 120 HisAlaMetMetLysArgGlyTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValIle 139
QY 355 GTCTCCTCA 363
Db 140 ValSerSer 142

QY 184 GCTCTCATGTCCAGACTGAGCATCAGCAAAAGACAACCTCAAGAGCCAAAGTTTCTTAAAA 243
Db 81 AlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeuLys 100
QY 244 ATGAACAGTCTGCAGACTGATGACACAGCCCATGTACTACTGTGCCAGAGAT----- 294
Db 101 MetAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgGluGlyGluphe 120
QY 295 -----CGATCTACTATGATTACGGCCTATCGCTATGGACTACTGGGGCCCAAGGGACC 345
Db 121 AspTyrTyrGlySerSerLeuLeuSerTyrHisSerMetAsnPheTrpGlyGlnGlyThr 140
QY 346 ACGGTCACCGTCTCCTCA 363
Db 141 SerValThrValSerSer 146

RESULT 7
US-08-973-518-4
; Sequence 4, Application US/08973518
; Publication No. US20010014327A1
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; APPLICANT: Barber, Brian H
; APPLICANT: Cates, George A
; APPLICANT: Caterini, Judith E
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,518
; FILING DATE: 07-APR-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-973-518-4

Alignment Scores:
Pred. No.: 8.63e-46 Length: 140
Score: 531.50 Matches: 103
Percent Similarity: 88.43% Conservative: 4
Best Local Similarity: 85.12% Mismatches: 13
Query Match: 78.97% Indels: 1
DB: 8 Gaps: 1

US-10-049-868A-2 (1-363) x US-08-973-518-4 (1-140)

QY 1 CAGGTGACGTGCAGGAGTCTGGACCTGGCTGGCGCCCTCACAGAGCCTGTCCATC 60
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Db 21 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 40
QY 61 ACTTGCACTGTCTCTGGGATTTCATTAAACAGATATGGTGTACACTGGGTTCCGACGCCT 120
Db 41 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 60
QY 121 CCAGGAAAGGGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCACAAATATATAAT 180
Db 61 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerIleAsnTyrAsn 80
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAACAGACAACTCCAAGAGCCCAAGTTTCTTTA 240
Db 81 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnPheLysSerGlnValPheLeu 100
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
Db 101 LysMetSerSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAlaTyrGly 120
QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCCAAGGGACCACGGTCACCGTCTCTCC 360
Db 121 AspTyrVal---HisTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrAlaSer 139
QY 361 TCA 363
Db 140 Ser 140

RESULT 8
US-09-007-093-4
; Sequence 4, Application US/09007093
; Patent No. US20020025315A1
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; APPLICANT: Barber, Brian H
; APPLICANT: Cates, George A
; APPLICANT: Caterini, Judith E
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,093
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,576
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-765
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-007-093-4

Alignment Scores: 8.63e-46 Length: 140
Pred. No.: 531.50 Matches: 103
Score: 531.50
Percent Similarity: 88.43% Conservative: 4
Best Local Similarity: 85.12% Mismatches: 13
Query Match: 78.97% Indels: 1
DB: 9 Gaps: 1

US-10-049-868A-2 (1-363) x US-09-007-093-4 (1-140)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
|||||:|||||
Db 21 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 40

QY 61 ACTTGCACCTCTCTGGGATTTCATTAAACAGATATGGTGTACACTGGGTTCCGCGCCT 120
|||||
Db 41 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 60

QY 121 CCAGGAAAGGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGGAAGCACAAATTATAAT 180
|||||
Db 61 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerIleAsnTyrAsn 80

QY 181 TCGGCTCTCATGTCCAGACTGATGACACAGCCACTGCTACTGTCAGAGCCAAAGTTTCTTA 240
|||||
Db 81 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnPheLysSerGlnValPheLeu 100

QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCACTGCTACTGTGCCAGAGATCGATCT 300
|||||:|||||
Db 101 LysMetSerSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAlaTyrGly 120

QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCAAGGACCACCGTCCCGTCTCC 360
:::|||||:|||||
Db 121 AspTyrVal---HisTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrAlaSer 139

QY 361 TCA 363
|||
Db 140 Ser 140

RESULT 9

US-10-428-754-4
; Sequence 4, Application US/10428754
; Publication No. US20030228304A1
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; Barber, Brian H
; Cates, George A
; Caterini, Judith E
; Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/428,754
; FILING DATE: 05-May-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 10/428,754
; FILING DATE: 05-MAY-2003
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-1065
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-428-754-4

Alignment Scores: 8.63e-46 Length: 140
Pred. No.: 531.50 Matches: 103
Score: 531.50
Percent Similarity: 88.43% Conservative: 4
Best Local Similarity: 85.12% Mismatches: 13
Query Match: 78.97% Indels: 1
DB: 14 Gaps: 1

US-10-049-868A-2 (1-363) x US-10-428-754-4 (1-140)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
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Db 21 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 40

QY 61 ACTTGCACCTCTCTGGGATTTCATTAAACAGATATGGTGTACACTGGGTTCCGCGCCT 120
|||||
Db 41 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnPro 60

QY 121 CCAGGAAAGGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGGAAGCACAAATTATAAT 180
|||||
Db 61 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerIleAsnTyrAsn 80

QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAATCAGCAAAAGACCAACTCCAGAGCCCAAGTTTCTTA 240
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Db 81 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnPheLysSerGlnValPheLeu 100

QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCACTGCTACTGTGCCAGAGATCGATCT 300
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Db 101 LysMetSerSerLeuGlnThrAspThrAlaMetTyrTyrCysAlaArgAlaTyrGly 120

QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCCAAGGACCACCGTCCCGTCTCC 360
:::|||||:|||||
Db 121 AspTyrVal---HisTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValThrAlaSer 139

QY 361 TCA 363
|||
Db 140 Ser 140

RESULT 10

US-10-232-187-2
; Sequence 2, Application US/10232187
; Publication No. US20030092091A1
; GENERAL INFORMATION:
; APPLICANT: Abrahamson, Julie A.
; APPLICANT: Bochner, Bruce
; APPLICANT: Erickson-Miller, Connie L.
; APPLICANT: Kikly, Kristine K.
; APPLICANT: Schleimer, Robert
; APPLICANT: Nulku, Turkan E.
; TITLE OF INVENTION: Sialoadhesin Factor-2 Antibodies
; FILE REFERENCE: GH50042-1
; CURRENT APPLICATION NUMBER: US/10/232,187
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/187,595
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: PCT/US01/07193
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/315,943
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/349,830

; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/394,741
; PRIOR FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-232-187-2

Alignment Scores:
Pred. No.: 9.54e-46 Length: 119
Score: 531.00 Matches: 104
Percent Similarity: 91.74% Conservative: 7
Best Local Similarity: 85.95% Mismatches: 8
Query Match: 78.90% Indels: 2
DB: 14 Gaps: 2

US-10-049-868A-2 (1-363) x US-10-232-187-2 (1-119)

QY 1 CAGGTGCAGCTGCAGAGTCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGTCTCTGGGATTTCATTAAACAGATATGGTGTACACTGGGTTCCGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeu--IleTyrGlyAlaHisTrpValArgGlnPro 39
QY 121 CCAGGAAAGGCTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGGAGCACAAATTATAAT 180
Db 40 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 59
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAAGAGCCCAAGTTTCTTA 240
Db 60 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 79
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTGTGCCAGAGATCGATCT 300
Db 80 LysIleAsnSerLeuGlnThrAspAspThrAlaLeuTyrTyrCysAlaArgAspGlySer 99
QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCAAAGGACCACGGTCACCGTCTCC 360
Db 100 SerProTyr--TyrTyrSerMetGluTyrTrpGlyGlnGlyThrSerValThrValSer 118
QY 361 TCA 363
Db 119 Ser 119

RESULT 11
US-10-239-656-23
; Sequence 23, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTTERBUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOFWEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23

; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Anti-NKG2D
; OTHER INFORMATION: hybridoma 6H7E7 variable heavy chain
US-10-239-656-23

Alignment Scores:
Pred. No.: 3.1e-45 Length: 119
Score: 526.00 Matches: 104
Percent Similarity: 86.78% Conservative: 1
Best Local Similarity: 85.95% Mismatches: 14
Query Match: 78.16% Indels: 2
DB: 15 Gaps: 1

US-10-049-868A-2 (1-363) x US-10-239-656-23 (1-119)

QY 1 CAGGTGCAGCTGCAGAGTCTGGACCTGGCCCTGGTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 1 GlnValGlnLeuGlnGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGTCTCTGGGATTTCATTAAACAGATATGGTGTACACTGGGTTCCGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrGlyValHisTrpIleArgGlnPro 40
QY 121 CCAGGAAAGGCTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGGAGCACAAATTATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsn 60
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAAGAGCCCAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTGTGCCAGAGATCGATCT 300
Db 81 LysMetAsnSerLeuGlnIleAspAspThrAlaMetTyrTyrCysAla-----ArgGly 98
QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCAAAGGACCACGGTCACCGTCTCC 360
Db 99 GlyTyrGluGlyAlaAlaTrpPheGlyTyrTrpGlyGlnGlyThrThrValThrValSer 118
QY 361 TCA 363
Db 119 Ser 119

RESULT 12
US-10-144-644-15
; Sequence 15, Application US/10144644
; Publication No. US20030059429A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/144,644
; FILING DATE: 2002-08-08
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION: INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-144-644-15

Alignment Scores:
Pred. No.: 6.3e-45 Length: 119
Score: 523.00 Matches: 100
Percent Similarity: 88.43% Conservative: 7
Best Local Similarity: 82.64% Mismatches: 12
Query Match: 77.71% Indels: 2
DB: 14 Gaps: 1

US-10-049-868A-2 (1-363) x US-10-144-644-15 (1-119)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20

QY 61 ACTTGCACTGTCTGGGATTTTCATTAACAGATATGGTGTACACTGGGTTCCGCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrSerValHisTrpValArgGlnPro 40

QY 121 CCAGGAAAGGTCCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCACACAATATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaSerGlyGlyThrAspTyrAsn 60

QY 181 TCGGCTCTCATGTCAGACTGAGCATCAGCAAGACAACACTCCAAGAGCCCAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80

QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCACAGATCGATCT 300
Db 81 LysLeuAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspProPro 100

QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGCGCAAGGACCACGGTCACCGTCTCC 360
Db 101 SerSerLeu-----LeuArgLeuAspTyrTrpGlyGlnGlyThrThrLeuThrValSer 118

QY 361 TCA 363
Db 119 Ser 119

RESULT 13
US-10-700-740-15
; Sequence 15, Application US/10700740
; Publication No. US20040156850A1
; GENERAL INFORMATION:

; APPLICANT: Ames, Robert S.
; Appelbaum, Edward R.
; Chaiken, Irwin M.
; Cook, Richard M.
; Gross, Mitchell S.
; Holmes, Stephen D.
; McMillan, Lynette J.
; Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/700,740
; FILING DATE: 04-Nov-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/144,644
; FILING DATE: 2002-08-08
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-700-740-15

Alignment Scores:
Pred. No.: 6.3e-45 Length: 119
Score: 523.00 Matches: 100
Percent Similarity: 88.43% Conservative: 7
Best Local Similarity: 82.64% Mismatches: 12
Query Match: 77.71% Indels: 2
DB: 16 Gaps: 1

US-10-049-868A-2 (1-363) x US-10-700-740-15 (1-119)

QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20

QY 61 ACTTGCACTGTCTGGGATTTTCATTAACAGATATGGTGTACACTGGGTTCCGCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrSerTyrSerValHisTrpValArgGlnPro 40

QY 121 CCAGGAAAGGTCCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCACACAATATAAT 180

Db 41 ProGlyLysGlyLeuGluTrpLeuGlyValIleTrpAlaSerGlyGlyThrAspTyrAsn 60
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAAGAGCCCAAGTTTCTTA 240
Db 61 SerAlaLeuMetSerArgLeuSerIleSerLysAspAsnSerLysSerGlnValPheLeu 80
QY 241 AAAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
Db 81 LysLeuAsnSerLeuGlnThrAspAspThrAlaMetTyrTyrCysAlaArgAspProPro 100
QY 301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCAAAGGACCACGGTCACCGTCTCC 360
Db 101 SerSerLeu-----LeuArgLeuAspTyrTrpGlyGlnGlyThrThrLeuThrValSer 118
QY 361 TCA 363
Db 119 Ser 119

RESULT 14
US-09-824-286-3
; Sequence 3, Application US/09824286
; Patent No. US20020028202A1
; GENERAL INFORMATION:
; APPLICANT: Burkly, Linda C
; Benjamin, Christopher D
; Hession, Catherine A
; Whitty, Adrian
; TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/824,286
; FILING DATE: 02-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,466
; FILING DATE: 10-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A006 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 679-2000
; TELEFAX: 617 679-2838
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Alignment Scores:
Pred. No.: 8.92e-45 Length: 112
Score: 521.50 Matches: 98
Percent Similarity: 92.17% Conservative: 8
Best Local Similarity: 85.22% Mismatches: 6
Query Match: 77.49% Indels: 3
DB: 9 Gaps: 1

US-10-049-868A-2 (1-363) x US-09-824-286-3 (1-112)
QY 10 CTGCAGGAGTCTGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACTTGCACT 69
Db 1 LeuGlnGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIleThrCysThr 20
QY 70 GTCTCTGGGATTTCATTAAACAGATATGGTGTAACCTGGGTTGCCAGCCTCCAGGAAAG 129
Db 21 ValSerGlyPheSerLeuThrSerTyrGlyValHisTrpValArgGlnProProGlyLys 40
QY 130 GGTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAAAGCACAATTTATAATTCGGCTCTC 189
Db 41 GlyLeuGluTrpLeuGlyValIleTrpAlaGlyGlySerThrAsnTyrAsnSerAlaLeu 60
QY 190 ATGTCCAGACTGAGCATCAGCAAAGACAACTCCAAGAGCCCAAGTTTCTTAAAAATGAAC 249
Db 61 MetSerArgLeuAsnIleAsnArgAspAsnSerLysSerGlnIlePheLeuLysMetAsn 80
QY 250 AGTCTGCAGACTGATGACACAGCCCATGTACTACTGTGCCAGAGATCGATCTACTATGATT 309
Db 81 SerLeuGlnThrAspAspThrAlaIleTyrTyrCysAlaArgGluGlySerThrVal--- 99
QY 310 ACGGCCTATGCTATGGACTACTGGGGCCAAAGGGACACGGTCACC 354
Db 100 -----AspSerMetAspTyrTrpGlyGlnGlyThrThrValThr 112

RESULT 15
US-10-207-655-252
; Sequence 252, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 252
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-252

Alignment Scores:
Pred. No.: 1.01e-44 Length: 121
Score: 521.00 Matches: 100
Percent Similarity: 88.43% Conservative: 7
Best Local Similarity: 82.64% Mismatches: 14
Query Match: 77.41% Indels: 0
DB: 14 Gaps: 0

US-10-049-868A-2 (1-363) x US-10-207-655-252 (1-121)
QY 1 CAGGTGCAGCTGCAGGAGTCTGGACCTGGCCTGGCGCCCTCACAGAGCCTGTCCATC 60
Db 1 GlnValGlnLeuLysGluSerGlyProGlyLeuValAlaProSerGlnSerLeuSerIle 20
QY 61 ACTTGCACTGTCTCTGGGATTTCATTAAACAGATATGGTGTAACCTGGGTTGCCAGCCT 120
Db 21 ThrCysThrValSerGlyPheSerLeuThrGlyTyrGlyValAsnTrpValArgGlnPro 40
QY 121 CCAGGAAAGGCTCTGGAGTGGCTGGGAGTAATATGGACTGGTGGAGCACAATATAAT 180
Db 41 ProGlyLysGlyLeuGluTrpLeuGlyMetIleTrpGlyAspGlySerThrAspTyrAsn 60
QY 181 TCGGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAACTCCAAGAGCCCAAGTTTCTTA 240
Db 61 SerAlaLeuLysSerArgLeuSerIleThrLysAspAsnSerLysSerGlnValPheLeu 80

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QY      241 AAATGAACAGTCTGCAGACTGATGACACAGCCATGTACTACTGTGCCAGAGATCGATCT 300
Db      81 LysMetAsnSerLeuGlnThrAspThrAlaArgTyrTyrCysAlaArgAspGlyTyr 100

QY      301 ACTATGATTACGGCCTATGCTATGGACTACTGGGGCCAAAGGACACCGGTACCGTCTCTCC 360
Db     101 SerAsnPheHisTyrTyrValMetAspTyrTrpGlyGlnGlyThrSerValThrValSer 120

QY      361 TCA 363
Db     121 Ser 121
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Search completed: October 13, 2004, 13:53:42
Job time : 72.3878 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 12:48:23 ; Search time 24.2958 Seconds
(without alignments)
471.266 Million cell updates/sec

Title: US-10-049-868A-3
Perfect score: 606
Sequence: 1 DIELTQSPAIMSPGKVT.....GTKLELKRADAAPTVSIFKL 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	460	75.9	235	2 S25058	Ig kappa chain - m
2	448	73.9	140	2 PL0013	Ig kappa chain pre
3	437	72.1	107	2 PC4405	Ig kappa chain V r
4	427	70.5	130	1 JL0079	Ig kappa chain pre
5	422	69.6	106	2 B54378	Ig light chain V r
6	422	69.6	107	2 A30562	Ig kappa chain V r
7	420	69.3	107	2 PD0011	Ig kappa chain V r
8	419	69.1	103	2 S29591	Ig kappa chain V r
9	419	69.1	132	2 S05268	Ig kappa chain pre
10	417	68.8	106	2 PS0071	Ig kappa chain V r
11	417	68.8	107	2 B30562	Ig kappa chain V r
12	416	68.6	106	2 G27887	Ig kappa chain V r
13	415	68.5	104	2 B49049	Ig kappa chain V r
14	413	68.2	107	2 S11119	Ig kappa chain V r
15	411	67.8	107	2 S11118	Ig kappa chain V r
16	405	66.8	107	2 S11121	Ig kappa chain V r
17	402.5	66.4	108	2 G30560	Ig kappa chain V r
18	401	66.2	107	2 PT0406	Ig kappa chain V r
19	400	66.0	107	2 PT0403	Ig light chain V r
20	399	65.8	107	2 S11112	Ig kappa chain V r
21	398	65.7	107	2 S11117	Ig kappa chain V r
22	396	65.3	107	2 PT0398	Ig light chain V r
23	394	65.0	104	2 JC6076	anti-D-dimer monoc
24	392	64.7	107	2 PT0402	Ig light chain V r
25	390	64.4	100	2 S29590	Ig kappa chain V r
26	389.5	64.3	106	2 S11114	Ig kappa chain V r
27	389	64.2	130	2 B32456	Ig kappa chain pre
28	386	63.7	107	2 PT0401	Ig light chain V r
29	385	63.5	106	2 PS0070	Ig kappa chain V r

30	385	63.5	120	2 A34871	Ig kappa chain V r
31	384	63.4	97	2 PH1084	Ig light chain V r
32	384	63.4	107	2 S11113	Ig kappa chain V r
33	384	63.4	107	2 PT0395	Ig light chain V r
34	384	63.4	130	2 S04573	Ig kappa chain pre
35	382	63.0	97	2 S26341	Ig light chain V r
36	382	63.0	107	2 S11116	Ig kappa chain V r
37	382	63.0	107	2 PT0400	Ig light chain V r
38	382	63.0	107	2 A42848	Ig light chain V r
39	380	62.7	107	2 S11123	Ig kappa chain V r
40	379	62.5	107	1 KVMSX4	Ig kappa chain V r
41	376.5	62.1	145	2 PL0014	Ig kappa chain pre
42	376	62.0	105	2 S26338	Ig kappa chain V r
43	376	62.0	107	2 PT0397	Ig light chain V r
44	376	62.0	130	2 A32513	Ig kappa chain pre
45	373	61.6	120	2 S66536	Ig light chain V r

ALIGNMENTS

RESULT 1
S25058
Ig kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C;Accession: S25058
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific
A;Reference number: S25057
A;Accession: S25058
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-235 <FIS>
A;Cross-references: EMBL:X67211; NID:g54828; PIDN:CAA47650.1; PID:g54829
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;38-111/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 460; DB 2; Length 235;
Best Local Similarity 79.3%; Pred. No. 5.2e-33;
Matches 92; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

Qy	2	IELTQSPAIMSPGKVTMTCSASSSVNYMHWFQESGTFPKRRIYDTSKLSGVVPARL 61
Db	24	IVLTQSPAIMSPGKVTMTCSASSSVSKMQWYQQXGTSFKRWIYDTSKLSGVPGRF 83
Qy	62	SGSGSGTEFTLEISRKAEADVGVVYCYQLVEYPLTFGAGTKLELKRADAAPTVSIF 117
Db	84	SGSGSGTSYSLTISSMEAEADAATYYCQQSSNPLTFGAGTKLELKRADAAPTVSIF 139

RESULT 2
PL0013
Ig kappa chain precursor V region (4C11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0013
R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A;Title: Structural basis of stimulatory anti-idiotypic antibodies.
A;Reference number: PL0011; MUID:88142863; PMID:3125424
A;Accession: PL0013
A;Molecule type: mRNA
A;Residues: 1-140 <CHE>
A;Experimental source: cell line 4C11
C;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylch

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
F;38-111/Domain: immunoglobulin homology <IMM>
F;46-55/Region: complementarity-determining 1

Query Match 68.8%; Score 417; DB 2; Length 106;
Best Local Similarity 78.1%; Pred. No. 1.3e-29;
Matches 82; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 2 IELTQSPAIMASPGKEKVTMTCSASSVNYMHWFQQESGTFPKRRIYDTSKLASGVPARL 61
Db 2 IVLTQSPAIMASPGKEKVTMTCSASSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARF 61

QY 62 SGSGSGTEFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLELK 106
Db 62 SGSGSGTSYSLTISMEAEADAATYYCQQWSSNPVTFGAPTKELEK 106

RESULT 11
B30562
Ig kappa chain V region (27.10.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C;Accession: B30562
R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L
J. Immunol. 142, 888-893, 1989
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bi
A;Reference number: A30562; MUID:89110066; PMID:2464031
A;Accession: B30562
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <SIK>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 417; DB 2; Length 107;
Best Local Similarity 75.5%; Pred. No. 1.4e-29;
Matches 80; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 2 IELTQSPAIMASPGKEKVTMTCSASSVNYMHWFQQESGTFPKRRIYDTSKLASGVPARL 61
Db 2 IVLTQSPAIMASPGKEKVTMTCSASSVSYMHWYQQKSGTSPKRWYDTSKLASGVPTRF 61

QY 62 SGSGSGTEFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLELKR 107
Db 62 SGSGSGTSYSLTISMEAEADAATYYCQQWSSNPVTFGGGTKLEIKR 107

RESULT 12
G27887
Ig kappa chain V region (H18-S415) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C;Accession: G27887
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a d
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: G27887
A;Molecule type: DNA
A;Residues: 1-106 <CAT>
A;Cross-references: UNIPROT:Q8VDD0
A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 416; DB 2; Length 106;
Best Local Similarity 76.2%; Pred. No. 1.6e-29;
Matches 80; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 2 IELTQSPAIMASPGKEKVTMTCSASSVNYMHWFQQESGTFPKRRIYDTSKLASGVPARL 61
Db 2 IVLTQSPAIMASPGKEKVTMTCSVSSISYMHWYQQKPGTSPKRWIYDTSKLASGVPTRF 61

QY 62 SGSGSGTEFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLELK 106
Db 62 SGRSGGTSFSLTISMEAEADAATYYCHQRSSYPLTFGAGTKLELK 106

RESULT 13
B49049
Ig kappa chain V region (anti-idiotypic) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B49049
R;Armandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.
Eur. J. Immunol. 22, 2893-2899, 1992
A;Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR anti
A;Reference number: A49049; MUID:93049629; PMID:1425914
A;Accession: B49049
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-104 <ARM>
A;Experimental source: BALB/c
A;Note: sequence extracted from NCBI backbone (NCBIN:118298, NCBIP:118299)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 68.5%; Score 415; DB 2; Length 104;
Best Local Similarity 78.6%; Pred. No. 2e-29;
Matches 81; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 2 IELTQSPAIMASPGKEKVTMTCSASSVNYMHWFQQESGTFPKRRIYDTSKLASGVPARL 61
Db 2 IVLTQSPAIMASPGKEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLTSQVPAF 61

QY 62 SGSGSGTEFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLE 104
Db 62 SGSGSGTSYSLTISMEAEADAATYYCQQWSSNPVTFGAGTKLE 104

RESULT 14
S11119
Ig kappa chain V region (clone NQ6-8.3.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C;Accession: S11119
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazol
A;Reference number: S07331; MUID:83271467; PMID:6877353
A;Accession: S11119
A;Molecule type: mRNA
A;Residues: 1-107 <NAT>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 413; DB 2; Length 107;
Best Local Similarity 76.4%; Pred. No. 3e-29;
Matches 81; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 2 IELTQSPAIMASPGKEKVTMTCSASSVNYMHWFQQESGTFPKRRIYDTSKLASGVPARL 61
Db 2 IVLTQSPXIMSXSPGKEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARF 61

QY 62 SGSGSGTEFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLELKR 107
Db 62 SGXGXGTSYSLTISSMFAEDAATYYCQQWSSNPVTFGAGTKLELKR 107

RESULT 15
S11118
Ig kappa chain V region (clone NQ5-61.1.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000

C;Accession: S11118
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A;Reference number: S07331; MUID:83271467; PMID:6877353
A;Accession: S11118
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <KAA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 67.8%; Score 411; DB 2; Length 107;
Best Local Similarity 77.4%; Pred. No. 4.5e-29;
Matches 82; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

Qy 2 IELTQSPAIMSASPGEKVTMTCSASSSVNYMHWFQQESGTFPKRRIYDTSKLASGVPARL 61

Db 2 IVLTQSPAIMSASPGEKVTMTCSASSSVNYMHWFQQESGTFPKRRIYDTSKLDGVPARF 61

Qy 62 SGSGSGTEFTLEISRKAEVGVYVCQQLVEYPLTFGAGTKLELKR 107

Db 62 SGSGSGTSYSLTISSMFAEDAATYCCQWSSNPLTFGAGTKLXLXR 107

Search completed: October 13, 2004, 13:00:06
Job time : 26.2958 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 12:47:33 ; Search time 119 Seconds
(without alignments)
575.375 Million cell updates/sec

Title: US-10-049-868A-3
Perfect score: 606
Sequence: 1 DIELTQSPAIMASPGKVT.....GTKLELKRADAAPTVSIFKL 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	452	74.6	112	2	Q8K1F2
2	451	74.4	235	2	Q91W12
3	444	73.3	134	2	Q8VDD0
4	433	71.5	112	2	Q8K1F0
5	421	69.5	107	1	KV6F_MOUSE
6	419	69.1	112	2	Q8K1F3
7	419	69.1	114	2	Q8K1F1
8	416	68.6	107	1	KV6I_MOUSE
9	415	68.5	107	1	KV6H_MOUSE
10	415	68.5	235	2	Q7TMK0
11	414	68.3	107	1	KV6G_MOUSE
12	411	67.8	111	2	AAR10981
13	411	67.8	111	2	AAR10982
14	411	67.8	111	2	AAR10994
15	410	67.7	108	2	AAR11048
16	409	67.5	110	2	AAR10999
17	408	67.3	107	1	KV6J_MOUSE
18	398	65.7	107	2	AAR11015
19	392	64.7	106	2	Q9U410
20	386	63.7	108	1	KV6K_MOUSE
21	385	63.5	107	1	KV6C_MOUSE
22	380	62.7	107	1	KV6B_MOUSE
23	379.5	62.6	214	2	Q9R1A5
24	379	62.5	107	1	KV6A_MOUSE
25	379	62.5	107	1	KV6D_MOUSE
26	377	62.2	111	2	AAR11009
27	374	61.7	106	2	AAR11006
28	373.5	61.6	236	2	Q7TS98
29	370	61.1	107	1	KV6E_MOUSE
30	368.5	60.8	131	2	Q811C3
31	366	60.4	97	2	AAR11055

32	364	60.1	92	2	AAR11066	Aar11066 mus muscu
33	364	60.1	95	2	AAR11062	Aar11062 mus muscu
34	360.5	59.5	114	2	AAR10983	Aar10983 mus muscu
35	358.5	59.2	234	2	Q8R062	Q8r062 mus musculu
36	358	59.1	111	2	AAR11021	Aar11021 mus muscu
37	356.5	58.8	234	2	Q8VCP0	Q8vcp0 mus musculu
38	355.5	58.7	237	2	Q7SZ36	Q7sz36 xenopus lae
39	354	58.4	129	1	KV4A_MOUSE	P01680 mus musculu
40	353.5	58.3	236	2	Q7Z3Y4	Q7z3y4 homo sapien
41	350.5	57.8	112	2	AAR11019	Aar11019 mus muscu
42	347.5	57.3	114	2	AAR11022	Aar11022 mus muscu
43	347.5	57.3	236	2	Q6PIH7	Q6pih7 homo sapien
44	347.5	57.3	236	2	Q6GMX9	Q6gmX9 homo sapien
45	347.5	57.3	236	2	AAH34141	Aah34141 homo sapi

ALIGNMENTS

RESULT 1

Q8K1F2					
ID	Q8K1F2	PRELIMINARY;	PRT;	112	AA.
AC	Q8K1F2;				
DT	01-OCT-2002 (Tremblrel. 22, Created)				
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)				
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)				
DE	Anti-VIPase light chain variable region (Fragment).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;				
RA	Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;				
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF516283; AAM64201.1; --				
DR	PIR; H33932; H33932.				
DR	HSSP; Q91W12; 1AY1.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig; 1.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
FT	NON_TER 1				
FT	NON_TER 112				
SQ	SEQUENCE 112 AA; 11953 MW; 4716B87FADB543ED CRC64;				

Query Match 74.6%; Score 452; DB 2; Length 112;
Best Local Similarity 78.6%; Pred. No. 5.5e-38;
Matches 88; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY	1	DIELTQSPAIMASPGKVTMTCSASSSVNVMHWFQESGTFPKRRIYDTSKLASGVPAR	60
Db	1	DIVLTQSPAIMASPGKVTITCNASSSVSYMHWFQKPGTSPKLIWYSTSNLASGVPAR	60
QY	61	LSGSGSGTEFTLEISRVAEDVGVIYCCQLVVEYPLTFGAGTKLELKRADAAP	112
Db	61	FSGSGSGTSYSLTISRMEADAATYYCQQRSSYPPLTFGAGTKLELKRADAAP	112

RESULT 2

Q91W12					
ID	Q91W12	PRELIMINARY;	PRT;	235	AA.
AC	Q91W12;				
DT	01-DEC-2001 (Tremblrel. 19, Created)				
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)				
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)				
DE	Hypothetical protein.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				

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RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N;
RA TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N;
RA TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
DR PDB; 1AY1; X-ray; L=23-232.
DR PDB; 1HQ4; X-ray; A/C=23-235.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 74.4%; Score 451; DB 2; Length 235;
Best Local Similarity 76.7%; Pred. No. 1.6e-37;
Matches 89; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTMTCSASSSVNYMHWFQQESGTFPKRRIYDTSKLAGVPARL 61
Db 24 IVLTQSPAIMSASPGERVMTCSASSSVSHMHVYQQKSGTSPKRWIYDTFKLTSGVPDRF 83

QY 62 SSGSGTGTEFTLEISRKAEADVGVVYCCQLVEYPLTFGAGTKLELKRADAAPT 117
Db 84 SSGSGGTSYSLTISNMEAEADVATYYCQWSRNPPTFGVGTGKLELKRADAAPT 139

RESULT 3
Q8VDD0 Q8VDD0 PRELIMINARY; PRT; 134 AA.
AC Q8VDD0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-MOG Z12 variable light chain (Fragment).
GN Name=anti-MOG kappa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

Query Match 74.4%; Score 451; DB 2; Length 235;
Best Local Similarity 76.7%; Pred. No. 1.6e-37;
Matches 89; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTMTCSASSSVNYMHWFQQESGTFPKRRIYDTSKLAGVPARL 61
Db 24 IVLTQSPAIMSASPGERVMTCSASSSVSHMHVYQQKSGTSPKRWIYDTFKLTSGVPDRF 83

QY 62 SSGSGTGTEFTLEISRKAEADVGVVYCCQLVEYPLTFGAGTKLELKRADAAPT 117
Db 84 SSGSGGTSYSLTISNMEAEADVATYYCQWSRNPPTFGVGTGKLELKRADAAPT 139

RESULT 3
Q8VDD0 Q8VDD0 PRELIMINARY; PRT; 134 AA.
AC Q8VDD0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-MOG Z12 variable light chain (Fragment).
GN Name=anti-MOG kappa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Sembi P.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Chernajovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416331; CAC94866.1; -.
DR PIR; G27887; G27887.
DR HSSP; P01834; 1MIM.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 134
SQ SEQUENCE 134 AA; 14525 MW; CDF8E2236E2D0CF CRC64;

Query Match 73.3%; Score 444; DB 2; Length 134;
Best Local Similarity 76.6%; Pred. No. 4.4e-37;
Matches 85; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSASPGKVTMTCSASSSVNYMHWFQQESGTFPKRRIYDTSKLAGVPARL 61
Db 24 IVLTQSPAIMSASPGKVTMTCSASSSVSHMHVYQQKPGTSPKRWIYDTSKLAGVPARF 83

QY 62 SSGSGTGTEFTLEISRKAEADVGVVYCCQLVEYPLTFGAGTKLELKRADAAP 112
Db 84 SSGSGGTSYSLTISNMEAEADAATYYCHQRSSYFPTFGGTTKLEIKRADAAP 134

RESULT 4
Q8K1F0 Q8K1F0 PRELIMINARY; PRT; 112 AA.
AC Q8K1F0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516285; AAM64203.1; -.
DR PIR; A33933; A33933.
DR PIR; PC4405; PC4405.
DR HSSP; P01837; 1ORQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 11901 MW; F6644663201AA239 CRC64;

Query Match 71.5%; Score 433; DB 2; Length 112;
Best Local Similarity 77.1%; Pred. No. 4.7e-36;
Matches 84; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTMTCSASSSVNYMHWFQQESGTFPKRRIYDTSKLAGVPARLSG 63
Db 4 LTQSPAIMSASPGKVTMTCSASSSVSHMHVYQQKSGTSPKRWIYDTSKLAGVPARFSG 63

QY 64 SSGSGTGTEFTLEISRKAEADVGVVYCCQLVEYPLTFGAGTKLELKRADAAP 112
RN [1]
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Db 64 SSGNSYSLTISTEGEDAATYYCQWSSNPPTFGGGTKLEIKRADAAP 112
RESULT 5
KV6F_MOUSE STANDARD; PRT; 107 AA.
AC P04940;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-17.4.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RL Nature 304:320-324(1983).
CC -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC -----
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CC -----
CC EMBL; K00735; AAA38680.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 33 Complementarity-determining-1.
FT DOMAIN 34 48 Framework-2.
FT DOMAIN 49 55 Complementarity-determining-2.
FT DOMAIN 56 87 Framework-3.
FT DOMAIN 88 96 Complementarity-determining-3.
FT DOMAIN 97 106 Framework-4.
FT DISULFID 23 87 By similarity.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11561 MW; 6F694284ECAF68E6 CRC64;
Query Match 69.5%; Score 421; DB 1; Length 107;
Best Local Similarity 77.4%; Pred. No. 7.4e-35;
Matches 82; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 2 IELTQSPAIMSASPGKVTMTCSASSSVNYMHWFQESGTFPKRRIYDTSKLASGVPARL 61
Db 2 IVLTQSPAIMSASPGQKVTMTCSASSSVNYMHWFQYQQSGTSPKRWIYDTSKLASGVPARF 61
QY 62 SSGSGTGTEFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLELKR 107
Db 62 SSGGSATSYSLTITSMQAEADAATYYCQWSSNPPLTFGAGTKLELKR 107
RESULT 6
Q8K1F3 PRELIMINARY; PRT; 112 AA.
AC Q8K1F3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516282; AAM64200.1; -.
DR PIR; A33933; A33933.
DR PIR; PH1085; PH1085.
DR HSSP; P01837; 25C8.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 112
FT NON_TER 112
SQ SEQUENCE 112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;
Query Match 69.1%; Score 419; DB 2; Length 112;
Best Local Similarity 72.3%; Pred. No. 1.2e-34;
Matches 81; Conservative 12; Mismatches 19; Indels 0; Gaps 0;
QY 1 DIELTQSPAIMSASPGKVTMTCSASSSVNYMHWFQESGTFPKRRIYDTSKLASGVPAR 60
Db 1 DIVLTQSPAIMSASPGKVTMTCSASSSVNYMWYQYQQKPGSSPKPWIYRTSNLASGVPAR 60
QY 61 LSGSGTGTEFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLELKRADAAP 112
Db 61 FSGSGSGTSYSLTITSSMEADAATYYCQYHSPYTFGGGTKLEIKRADAAP 112
RESULT 7
Q8K1F1 PRELIMINARY; PRT; 114 AA.
AC Q8K1F1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516284; AAM64202.1; -.
DR PIR; A33933; A33933.
DR PIR; PH1058; PH1058.
DR HSSP; P01837; 25C8.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 114
FT NON_TER 114
SQ SEQUENCE 114 AA; 12162 MW; 8BD9833DBF3EEFD1 CRC64;
Query Match 69.1%; Score 419; DB 2; Length 114;
Best Local Similarity 72.8%; Pred. No. 1.3e-34;
Matches 83; Conservative 9; Mismatches 20; Indels 2; Gaps 1;
QY 1 DIELTQSPAIMSASPGKVTMTCSASSSV--NYMHWFQESGTFPKRRIYDTSKLASGV 58
Db 1 DIVLTQSPAIMSASPGKVTMTCRASSSVSSSYLHWYQQKSGSPKLIWYSTSNLASGV 60
QY 59 ARLSGSGTGTEFTLEISRKAEDVGYYCQQLVEYPLTFGAGTKLELKRADAAP 112
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Db 61 ARFSGSGSGTYSLSLTISMEAEADAATYYCQYHSYPRTFGGGKLEIKRADAAP 114

RESULT 8

KV6I MOUSE

ID_KV6I_MOUSE STANDARD; PRT; 107 AA.

AC P04943;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-VI region NQ6-8.3.1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83271467; PubMed=6877353;

RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;

RT "mRNA sequences define an unusually restricted Igg response to 2-phenylloxazolone and its early diversification.";

RL Nature 304:320-324(1983).

CC -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.

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CC

CC

DR EMBL; K00740; AAA38685.1; -.

DR HSSP; P01679; 2FBJ.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Hybridoma; Immunoglobulin V region.

FT DOMAIN 1 23 Framework-1.

FT DOMAIN 24 33 Complementarity-determining-1.

FT DOMAIN 34 48 Framework-2.

FT DOMAIN 49 55 Complementarity-determining-2.

FT DOMAIN 56 87 Framework-3.

FT DOMAIN 88 96 Complementarity-determining-3.

FT DOMAIN 97 106 Framework-4.

FT DISULFID 23 87 By similarity.

FT NON_TER 107 107

SQ SEQUENCE 107 AA; 11572 MW; 6F694824ECFC9B6 CRC64;

Query Match 68.6%; Score 416; DB 1; Length 107;

Best Local Similarity 76.4%; Pred. No. 2.4e-34;

Matches 81; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 2 IELTQSPAIMASPGKVTMTCSASSSVNYMHWFQESGTFPKRRIYDTSKLASGVPARL 61

Db 2 IVLTQSPAIMASPGQKVTMTCSASSSVNYMHWYQKSGTSPKRWIYDTSKLASGXPARF 61

QY 62 SGSGSGTEFTLEISRKAEADVGVYCCQLVEYPLTFGAGTKLELKR 107

Db 62 SGSGSATSYSLTITSMQAEADAATYYCQWSSNPLTFGAGTKLELKR 107

RESULT 9

KV6H MOUSE

ID_KV6H_MOUSE STANDARD; PRT; 107 AA.

AC P04942;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-VI region NQ5-61.1.2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83271467; PubMed=6877353;

RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;

RT "mRNA sequences define an unusually restricted Igg response to 2-phenylloxazolone and its early diversification.";

RL Nature 304:320-324(1983).

CC -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.

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CC

CC

DR EMBL; K00739; AAA38684.1; -.

DR HSSP; P01679; 2FBJ.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Hybridoma; Immunoglobulin V region.

FT DOMAIN 1 23 Framework-1.

FT DOMAIN 24 33 Complementarity-determining-1.

FT DOMAIN 34 48 Framework-2.

FT DOMAIN 49 55 Complementarity-determining-2.

FT DOMAIN 56 87 Framework-3.

FT DOMAIN 88 96 Complementarity-determining-3.

FT DOMAIN 97 106 Framework-4.

FT DISULFID 23 87 By similarity.

FT NON_TER 107 107

SQ SEQUENCE 107 AA; 11605 MW; CA6C4284BCFCB550 CRC64;

Query Match 68.5%; Score 415; DB 1; Length 107;

Best Local Similarity 76.4%; Pred. No. 3e-34;

Matches 81; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 2 IELTQSPAIMASPGKVTMTCSASSSVNYMHWFQESGTFPKRRIYDTSKLASGVPARL 61

Db 2 IVLTQSPAIMASPGQKVTMTCSASSSVNYMHWYQKSGTSPKRWIYDTSKLDGVPARF 61

QY 62 SGSGSGTEFTLEISRKAEADVGVYCCQLVEYPLTFGAGTKLELKR 107

Db 62 SGSGSATSYSLTITSMQAEADAATYYCQWSSNPLTFGAGTKLELKR 107

RESULT 10

Q7TMK0

ID_Q7TMK0 PRELIMINARY; PRT; 235 AA.

AC Q7TMK0;

DT 01-OCT-2003 (TReMBLrel. 25, Created)

DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Hypothetical protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CZECH II;

RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/wnt1 model.

RC Expression driven by an MMTV-LTR enhancer.;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,


```
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBBJ databases.
DR EMBL; BC055911; AAH55911.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25861 MW; 3EBA0312A87613F4 CRC64;

Query Match 68.5%; Score 415; DB 2; Length 235;
Best Local Similarity 72.8%; Pred. No. 7.4e-34;
Matches 83; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

QY 4 LTQSPAIMASAPGKVTMTCSASSSVNYMHWFQESGTFPKRRIYDTSKLASGVPARLSG 63
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
26 LTQSPAIMASASLGKVTMTSCASSRVNYMYWYQQKSGASPKLWIYYTSLNAPGVPARFSG 85

QY 64 SSGSGTEFTLEISRKAEADVGVYCCQLVEYPLTFGAGTKLELKRADAAPTIVSIF 117
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
86 SSGSGTSYSLTISVVEAEADAATYYCQQLSTSPWTFGGSKLEIKRADAAPTIVSIF 139

RESULT 11
KV6G MOUSE
ID _KV6G MOUSE STANDARD; PRT; 107 AA.
AC P04941;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-48.2.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
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CC -----
DR EMBL; K00737; AAA38682.1; -.
DR HSSP; Q91W12; IAY1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 33 Complementarity-determining-1.
FT DOMAIN 34 48 Framework-2.
FT DOMAIN 49 55 Complementarity-determining-2.
FT DOMAIN 56 87 Framework-3.
FT DOMAIN 88 96 Complementarity-determining-3.
FT DOMAIN 97 106 Framework-4.
FT DISULFID 23 87 By similarity.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11556 MW; 72488DA9EF354934 CRC64;

Query Match 68.3%; Score 414; DB 1; Length 107;
Best Local Similarity 76.4%; Pred. No. 3.8e-34;
Matches 81; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 2 IELTQSPAIMASAPGKVTMTCSASSSVNYMHWFQESGTFPKRRIYDTSKLASGVPARL 61
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2 ILLTQSPAIMASAPGKVTMTCSASSSVNYMHWFQKSGTSPKRWIYDTSKLASGVPARF 61

QY 62 SSGSGTEFTLEISRKAEADVGVYCCQLVEYPLTFGAGTKLELKR 107
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
62 SSGGSATSYSLTITSMQAEADAATYYCQQWSSNPLTFGAGTKLXLKR 107

RESULT 12
AAR10981
ID AAR10981 PRELIMINARY; PRT; 111 AA.
AC AAR10981;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.Sle1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.Sle1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBBJ databases.
DR EMBL; AY436821; AAR10981.1; -.
FT NON_TER 1 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 11819 MW; EE2F666368BC91BC CRC64;

Query Match 67.8%; Score 411; DB 2; Length 111;
Best Local Similarity 71.8%; Pred. No. 7.9e-34;
Matches 79; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 4 LTQSPAIMASAPGKVTMTCSASSSVNYMHWFQESGTFPKRRIYDTSKLASGVPARLSG 63
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2 MTQTPTILSAPGKVTMTCRASSSVNYMHWFQKPGSSPKWIYATSNLASGVPARFSG 61

QY 64 SSGSGTEFTLEISRKAEADVGVYCCQLVEYPLTFGAGTKLELKRADAAPT 113
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
62 SSGSGTSYSLTISVVEAEADAATYYCQQWSSNPPPTFGGKLEIKRADAAPT 111
```


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OM protein - protein search, using sw model

Run on: October 13, 2004, 12:44:23 ; Search time 111.067 Seconds
(without alignments)
384.353 Million cell updates/sec

Title: US-10-049-868A-3
Perfect score: 606
Sequence: 1 DIELTQSPAIMASPGKVT.....GTKLELKRADAAPTVSIFKL 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	471	77.7	215	7	ADE06764
2	466	76.9	144	8	ADM79827
3	460	75.9	135	2	AAR08347
4	459	75.7	129	5	ABB75616
5	458	75.6	235	2	AAW41392
6	452	74.6	108	2	AAR21301
7	452	74.6	156	8	ADO43520
8	451	74.4	215	2	AAR43674
9	451	74.4	215	2	AAR99644
10	451	74.4	215	2	AAR97377
11	448	73.9	108	2	AAR21293
12	445	73.4	235	2	AAR13060
13	444	73.3	241	6	ABR62010
14	444	73.3	255	3	AAB11398
15	444	73.3	255	4	AAB74199
16	444	73.3	255	4	AAB70769
17	444	73.3	255	4	AAY72020
18	443.5	73.2	214	2	AAW15933
19	443	73.1	118	6	AAE37758
20	443	73.1	118	6	AAE37807
21	441	72.8	316	2	AAY32086
22	439	72.4	108	2	AAR21303
23	439	72.4	108	2	AAW41388
24	439	72.4	266	8	ADH77307
25	439	72.4	309	4	AAB70841

26	437	72.1	236	2	AAAY34096	Partial a
27	437	72.1	241	2	ABB76197	Anti-meso
28	437	72.1	241	4	AAB50019	Antimesot
29	437	72.1	288	2	AAW82482	Mouse bis
30	437	72.1	539	3	AAAY50823	Fv-antibo
31	437	72.1	554	3	AAAY50822	Fv-antibo
32	437	72.1	562	6	ABR57059	Plasmid p
33	436	71.9	109	6	ABU63531	Anti-cucu
34	435	71.8	108	2	AAR21294	Murine VL
35	435	71.8	108	2	AAR21292	Murine VL
36	435	71.8	330	4	AAB70842	SNV-env 1
37	434.5	71.7	208	2	AAAY44175	MAB FabI3
38	433	71.5	108	2	AAR79884	Anti-EGFR
39	433	71.5	108	3	AAB12461	IGG monoc
40	433	71.5	241	5	AAW48925	scFv anti
41	432	71.3	108	3	AAAY97236	Variable
42	432	71.3	108	4	AAAB82710	VEGF anta
43	432	71.3	108	5	AAE25956	Mouse ant
44	432	71.3	108	5	AAU74413	Antigen-b
45	432	71.3	108	6	ABJ26725	VEGF bind

ALIGNMENTS

RESULT 1
ADE06764
ID ADE06764 standard; protein; 215 AA.
XX
AC ADE06764;
XX
DT 29-JAN-2004 (first entry)
XX
DE D18 light chain protein SEQ ID NO:34.
XX
KW hybrid polypeptide; protein aggregation; prion polypeptide;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant;
KW cerebroprotective; antiparkinsonian; cytosstatic; nephrotropic; cardiant;
KW antiinflammatory; antiarteriosclerotic; gene therapy;
KW Creutzfeldt-Jakob disease; scrapie and bovine spongiform encephalopathy;
KW Alzheimer's disease; Type II diabetes; Huntington's disease;
KW immunoglobulin amyloidosis; amyloidosis; chronic inflammatory disease;
KW amyotrophic lateral sclerosis; Pick's disease; Parkinson's disease;
KW Frontotemporal dementia; multiple myeloma; plasma cell dyscrasia;
KW familial amyloidotic polyneuropathy; medullary carcinoma;
KW chronic renal failure; congestive heart failure; chronic inflammation;
KW atherosclerosis.
XX
OS Synthetic.
XX
PN WO2003085086-A2.
XX
PD 16-OCT-2003.
XX
PF 08-APR-2003; 2003WO-US010856.
XX
PR 09-APR-2002; 2002US-0371610P.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Burton DR, Williamson RA, Moroncini G;
XX
DR WPI; 2003-877028/81.
XX
DR N-PSDB; ADE06763.
XX
PT New motif-grafted hybrid polypeptides binding to the infectious form of a
PT prion, useful for diagnosing or treating diseases of protein aggregation
PT or conformation, e.g. amyloidosis, Alzheimer's disease, renal failure or
PT diabetes.
XX
PS Disclosure; SEQ ID NO 34; 115pp; English.
XX
CC The present invention describes a hybrid polypeptide (I) comprising: (a)

Query Match 74.6%; Score 452; DB 2; Length 108;
Best Local Similarity 81.5%; Pred. No. 4.3e-28;
Matches 88; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTMTCSASSSVNYMHWFQESGTFPKRRIYDTSKLAGVVPAR 60
Db 1 DIELTQSPAIMASPGKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLAGVVPAR 60

QY 61 LSGSGSGTEFTLEISRKAEADVGVYYCQQLVEYPLTFGAGTKLELKRA 108
Db 61 FSGSGSGTSYSLTISSEAEADVATYYCQQWSSNPLTFGAGTKLEIKRA 108

RESULT 7
ADO43520
ID ADO43520 standard; protein; 156 AA.
AC ADO43520;
XX
DT 29-JUL-2004 (first entry)
XX
DE Amino acid sequence of variable light chain of antibody BF11.
XX
KW antibody; lipase; biocatalysis; bioconversion; fragrance; flavour;
KW detergent; light chain; monoclonal antibody BF11.
XX
OS Mus musculus.
XX
PN WO2004039845-A1.
XX
PD 13-MAY-2004.
XX
PF 31-OCT-2002; 2002WO-EP012149.
XX
PR 31-OCT-2002; 2002WO-EP012149.
XX
PA (UYRO-) UNIV ROMA DEGLI STUDI LA SAPIENZA.
XX
PI Frati L, Biffoni M, Rughetti A, Koshkaki HR, Barachini S, Nuti M;
PI Palocci C, Soro S, Cernia E;
XX
DR WPI; 2004-376166/35.
DR N-PSDB; ADO43519.
XX
PT New antibodies and polypeptides that recognize microbial lipases and
PT enhance the hydrolytic activity of the enzyme, useful for e.g.
PT biocatalysis or bioconversion reactions, in biosensor technology or
PT bioremediation.
XX
PS Claim 11; Page 32; 42pp; English.
XX
CC The specification describes antibodies or polypeptides for microbial
CC lipase, which enhance the hydrolytic activity of the enzyme. The
CC polypeptides, antibodies or immunocomplex are useful for biocatalysis or
CC bioconversion reactions (e.g. hydrolysis, interesterification,
CC esterification, alcoholysis, acidolysis or aminolysis); in biosensor
CC technology; in bioremediation; in preparing fragrances or flavours and in
CC chemical modification of alcohols, acids, esters or fats; in cosmetic,
CC pharmaceutical and food industries; in preparing detergents; or in
CC identifying, purifying or measuring microbial lipases. The present
CC sequence represents the variable light chain of monoclonal antibody BF11,
CC which is directed against the Candida rugosa lipase.
XX
SQ Sequence 156 AA;

Query Match 74.6%; Score 452; DB 8; Length 156;
Best Local Similarity 75.2%; Pred. No. 6.1e-28;
Matches 88; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTMTCSASSSVNYMHWFQESGTFPKRRIYDTSKLAGVVPAR 60
Db 1 ELVLQSPAIMASPGKVTMTCSASSSVRIHWYQQKSGTSPKRWIYVTSKRASGVVPAR 60

QY 61 LSGSGSGTEFTLEISRKAEADVGVYYCQQLVEYPLTFGAGTKLELKRAAAPTVSIF 117
Db 61 FSGSGSGTSYSLTISSEAEADAATYYCQQWSSNPFTFGSGTKLEIKRAAAPTVSIF 117

RESULT 8
AAR43674
ID AAR43674 standard; protein; 215 AA.
XX
AC AAR43674;
XX
DT 25-MAR-2003 (revised)
DT 23-MAY-1994 (first entry)
XX
DE Mouse anti-bovine growth hormone MAb light chain.
XX
KW Monoclonal antibody; MAb; affinity; binding; antigen; diagnostics;
KW therapy; imaging; purification; biosensors.
XX
OS Mus musculus.
XX
PN US5260203-A.
XX
PD 09-NOV-1993.
XX
PF 25-APR-1990; 90US-00512910.
XX
PR 02-SEP-1986; 86US-00902971.
PR 02-SEP-1987; 87US-00092110.
PR 19-JAN-1989; 89US-00299617.
XX
PA (ENZO-) ENZON LABS INC.
XX
PI Ladner RC, Bird RE, Hardman K;
XX
DR WPI; 1993-367875/46.
DR N-PSDB; AAQ51535.
XX
PT Single chain poly:peptide for binding antigen - comprising light and
PT heavy chain antigen binding portions linked by peptide linker.
XX
PS Disclosure; Fig 22; 78pp; English.
XX
CC This sequence is the mature light chain of a monoclonal antibody (MAB)
CC and is the starting material for the production of a single chain
CC polypeptide having binding affinity for a given antigen (Bovine growth
CC hormone). The polypeptide comprises a first polypeptide comprising the
CC antigen binding portion of of the light chain variable region of an
CC antibody and a second polypeptide comprising the antigen binding portion
CC of the heavy chain variable region of an antibody and at least one
CC peptide linker linking the first and second polypeptide chains. The
CC resulting single chain polypeptide can be used in diagnostics, therapy
CC (in vivo and in vitro), imaging, purifications and biosensors. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PA field.)
XX
SQ Sequence 215 AA;

Query Match 74.4%; Score 451; DB 2; Length 215;
Best Local Similarity 78.4%; Pred. No. 1e-27;
Matches 91; Conservative 6; Mismatches 17; Indels 2; Gaps 1;

QY 4 LTQSPAIMASPGKVTMTCSASSSV--NYMHWFQESGTFPKRRIYDTSKLAGVVPARL 61
Db 4 LTQSPAIMASPGKVTMTCRASSSVSSSYLHWFQKSGASPKLWIYSTNLASGVPARF 63

QY 62 SGSGSGTEFTLEISRKAEADVGVYYCQQLVEYPLTFGAGTKLELKRAAAPTVSIF 117
Db 64 SGSGSGTSYSLTISSEAEADAATYYCQQYCSGYPLTFGAGTKLELKRAAAPTVSIF 119

RESULT 9
AAR99644

ID AAR99644 standard; protein; 215 AA.
XX AC AAR99644;
XX DT 25-MAR-2003 (revised)
DT 11-OCT-1996 (first entry)
XX DE Anti-bGH monoclonal antibody light chain.
XX KW Antibody engineering; single polypeptide chain binding molecule;
KW heavy chain; light chain; monoclonal antibody; MAb;
KW bovine growth hormone; bGH; immunoaffinity purification.
XX OS Mus sp.
XX PN US5534621-A.
XX PD 09-JUL-1996.
XX PF 06-JUN-1995; 95US-00468992.
XX PR 02-SEP-1986; 86US-00902971.
PR 02-SEP-1987; 87US-00092110.
PR 19-JAN-1989; 89US-00299617.
PR 25-APR-1990; 90US-00512910.
PR 01-APR-1993; 93US-00040440.
XX PA (ENZO-) ENZON LABS INC.
XX PI Bird RE, Ladner RC, Hardman K;
XX WPI; 1996-333309/33.
DR N-PSDB; AAT13734.
XX PT Immuno-purificn. using single binding chain molecule including antigen-
PT binding parts of antibody light and heavy chain variable regions
PT connected by a linker - is smaller, stabler and less expensive than
PT complete antibodies.
XX PS Example; Fig 22; 78pp; English.
XX SS The mature heavy chain (AAR99643) and mature light chain (AAR99644) of
CC the mouse anti-bovine growth hormone monoclonal antibody 3C2 can be
CC utilised in novel single chain binding molecules (AAR99645-48), in which
CC the hypervariable regions from IgG1 3C2 MAb are joined by peptide linkers
CC derived from the Fv regions of an IgA class anti- phosphorylcholine
CC myeloma antibody, MCPC-603. The single chain molecules retain the binding
CC specificity of the light and heavy chains and have the advantages of
CC smaller size, greater stability and reduced cost. They can be used in
CC therapy, diagnostics, imaging, purification and biosensors. (Updated on
CC 25-MAR-2003 to correct PF field.)
XX SQ Sequence 215 AA;
Query Match 74.4%; Score 451; DB 2; Length 215;
Best Local Similarity 78.4%; Pred. No. 1e-27;
Matches 91; Conservative 6; Mismatches 17; Indels 2; Gaps 1;
QY 4 LTQSPAIMASPGKVTMTCSASSV--NYMHWFQESGTFPKRRIYDTSKLASGVPARL 61
Db 4 LTQSPAIMASPGKVTMTCRASSSVSSSYLHWFQKSGASPKLWIYSTSNLASGVPARF 63
QY 62 SGSGSGTEFTLEISRKAEADVGVYQCQLVEYPLTFGAGTKLELKRADAAPTVSIF 117
Db 64 SGSGSGTSYSLTISSVBAEDAATYYCQYSGYPLTFGAGTKLELKRADAAPTVSIF 119
RESULT 10
AAR97377
ID AAR97377 standard; protein; 215 AA.
XX AC AAR97377;
XX

DT 25-MAR-2003 (revised)
DT 13-NOV-1996 (first entry)
XX XX Murine anti-BGH MAb light chain.
DE Antibody engineering; monoclonal antibody; MAb; light chain;
KW single chain antibody; immunoassay; bovine growth hormone; BGH.
XX OS Mus musculus.
XX PN US5518889-A.
XX PD 21-MAY-1996.
XX PF 06-JUN-1995; 95US-00468988.
XX PR 02-SEP-1986; 86US-00902971.
PR 02-SEP-1987; 87US-00092110.
PR 19-JAN-1989; 89US-00299617.
PR 25-APR-1990; 90US-00512910.
PR 01-APR-1993; 93US-00040440.
XX (ENZO-) ENZON LABS INC.
XX PI Bird RE, Ladner RC, Hardman K;
XX WPI; 1996-259060/26.
DR N-PSDB; AAT29057.
XX PT Immunoassay using single chain antigen binding mol. - as replacement for
PT labelled or immobilised antibody, are less immunogenic, easier to
PT engineer, more stable and less expensive.
XX PS Example 1; Fig 22; 78pp; English.
XX CC Portions of the heavy chain (AAR97376) and light chain (AAR97377) of
CC murine IgG1 anti-bovine growth hormone monoclonal antibody 3C2 can be
CC incorporated into novel single polypeptide chain binding molecules (see
CC also AAW02188-90). These are expressed in host cells using DNA constructs
CC (see also AAT36460-62) that include heavy and light chain encoding
CC sequences (AAT29056 and AAT29057) joined by linker moieties. Following
CC expression and refolding, the single chain binding molecules show the
CC binding characteristics of the aggregate of the 2 original heavy and
CC light chains of the variable region of the antibody. (Updated on 25-MAR-
XX 2003 to correct PF field.)
SQ Sequence 215 AA;
Query Match 74.4%; Score 451; DB 2; Length 215;
Best Local Similarity 78.4%; Pred. No. 1e-27;
Matches 91; Conservative 6; Mismatches 17; Indels 2; Gaps 1;
QY 4 LTQSPAIMASPGKVTMTCSASSV--NYMHWFQESGTFPKRRIYDTSKLASGVPARL 61
Db 4 LTQSPAIMASPGKVTMTCRASSSVSSSYLHWFQKSGASPKLWIYSTSNLASGVPARF 63
QY 62 SGSGSGTEFTLEISRKAEADVGVYQCQLVEYPLTFGAGTKLELKRADAAPTVSIF 117
Db 64 SGSGSGTSYSLTISSVBAEDAATYYCQYSGYPLTFGAGTKLELKRADAAPTVSIF 119
RESULT 11
AAR21293
ID AAR21293 standard; protein; 108 AA.
XX AC AAR21293;
XX DT 21-MAY-1992 (first entry)
XX DE Murine VL kappa group IV/VI chain h specific for phOx.
KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
KW g3p; binding; adsorption; gene VIII; diverse repertoire;

AC ABR62010;
XX
DT 03-OCT-2003 (first entry)
XX
DE Single-chain (scFv) antibody.
XX
KW Transgenic; biomolecule; ATP; ADP; cytostatic; virucide; gene therapy;
KW antisense therapy; scFv; antibody.
XX
OS Synthetic.
XX
PN EP1321524-A1.
XX
PD 25-JUN-2003.
XX
PF 19-DEC-2001; 2001EP-00130319.
XX
PR 19-DEC-2001; 2001EP-00130319.
XX
PA (DUER/) DUERING K.
XX
XX Mahn A, Hantke S, Petsch D;
PI
XX WPI; 2003-543829/52.
DR N-PSDB; ACC84876.
XX
PT Increasing the content of transgene-coded biomolecules in a plant or
PT animal, useful for producing proteins for diagnosing, preventing and/or
PT treating viral diseases and cancer, comprises changing the distribution
PT of ATP and/or ADP.
XX
PS Example 2; Fig 2; 18pp; English.
XX
XX The invention relates to increasing the content of one or more transgene-
CC coded biomolecules in an organism and involves changing the distribution
CC of ATP and/or ADP in cells of the organism. The yield of transgenic
CC molecules in host cells is often insufficient for industrial production.
CC The method increases the yield of transgenic molecules in animal and
CC plant host cells, therefore facilitating their production on an
CC industrial scale. The proteins produced by the method are useful for
CC diagnosing, preventing and/or treating viral diseases and cancer. The
CC present sequence represents a single-chain (scFv) antibody, used to
CC exemplify the increase in the expression of scFv antibodies in transgenic
CC potato tubers
XX
SQ Sequence 241 AA;

Query Match 73.3%; Score 444; DB 6; Length 241;
Best Local Similarity 80.0%; Pred. No. 4e-27;
Matches 88; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTMTCSASSSVNYMHWFQQESGTFPKRRIYDTSKLASGVPAR 60
Db 132 DIELTQSPAIMSASPGKVTMTCSASSSVRYNMWFFQKSGTSPKRWIYDTSKLSSGVPAR 191

QY 61 LSGSGSGTEFTLEISRVAEDVGYYCCQLVEYPLTFGAGTKLELKRAA 110
Db 192 FSGSGSGTSYSLTSSMEADAATYYCQOWSSNPLTFGAGTKLELKRAA 241

RESULT 14
AAB11398
ID AAB11398 standard; protein; 255 AA.
XX
AC AAB11398;
XX
DT 22-FEB-2001 (first entry)
XX
DE E. coli expression plasmid pUBS520-ScFvOx encoded protein.
XX
KW Eukaryotic protein; protease; interferon; antibody; hormone;
KW disulfide bridge.
XX

OS Escherichia coli.
OS Synthetic.
XX
PN EP1048732-A1.
XX
PD 02-NOV-2000.
XX
XX 26-APR-1999; 99EP-00107412.
PF
XX 26-APR-1999; 99EP-00107412.
PR
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA
XX WPI; 2000-674185/66.
DR N-PSDB; AAC66074.
XX
PT Preparation of water-soluble eukaryotic polypeptides with disulfide
PT bridges e.g. rPA, comprises cultivation of prokaryotic cells in the
PT presence of arginine or amide compound.
XX
XX Example 6; Page 22-23; 40pp; German.
PS
XX This invention describes a novel preparation of a water-soluble,
CC naturally occurring eukaryotic polypeptide containing two or more
CC cysteine units bound via a disulfide bridge which comprises cultivation
CC of prokaryotic cells in the presence of arginine or an amide compound.
CC The method is useful for the preparation of eukaryotic proteins e.g.
CC proteases, interferons, protein hormones, antibodies or antibody
CC fragments (e.g. a single chain FV fragment that binds to thyroid
CC stimulating hormone). It is especially useful for preparing proteins with
CC more than five disulfide bridges, e.g. recombinant plasminogen activator
CC (rPA). The technique is simple and does not require in vitro after-
CC treatment, such as the removal of inclusion bodies, reduction or
CC naturization
XX
SQ Sequence 255 AA;

Query Match 73.3%; Score 444; DB 3; Length 255;
Best Local Similarity 80.0%; Pred. No. 4.2e-27;
Matches 88; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTMTCSASSSVNYMHWFQQESGTFPKRRIYDTSKLASGVPAR 60
Db 132 DIELTQSPAIMSASPGKVTMTCSASSSVRYNMWFFQKSGTSPKRWIYDTSKLSSGVPAR 191

QY 61 LSGSGSGTEFTLEISRVAEDVGYYCCQLVEYPLTFGAGTKLELKRAA 110
Db 192 FSGSGSGTSYSLTSSMEADAATYYCQOWSSNPLTFGAGTKLELKRAA 241

RESULT 15
AAB74199
ID AAB74199 standard; protein; 255 AA.
XX
AC AAB74199;
XX
DT 29-MAY-2001 (first entry)
XX
DE PelB-scFvOxazolon fusion protein.
XX
KW Molecular chaperone; PelB signal sequence; scFvOxazolon.
XX Unidentified.
XX
PN EP1077262-A1.
XX
PD 21-FEB-2001.
XX
XX 24-JUL-2000; 2000EP-00115839.
PF
XX 29-JUL-1999; 99EP-00114811.
PR
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX
PI Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;
XX
DR WPI; 2001-246712/26.
DR N-PSDB; AAF77806.
XX
PT Producing naturally folded eukaryotic proteins e.g. antibodies,
PT interferon, hormones or proteases that contain two or several cysteines
PT linked by disulfide bridges comprises co-expression of a molecular
PT chaperone.
XX
PS Disclosure; Page 19; 35pp; English.
XX
CC The present invention relates to a method for production of a naturally
CC folded eukaryotic protein containing two or more cysteines linked by
CC disulfide bridges. The method comprises co-expression and secretion into
CC the periplasm of a molecular chaperone via an expression vector coding
CC for the chaperone. The expression vector also encodes a signal sequence.
CC The method is useful for producing a naturally folded eukaryotic protein
CC such as an antibody, antibody fragment, interferon, protein hormone or a
CC protease containing two or several cysteines linked by disulfide bridges.
CC The present sequence is a fusion protein composed of the PelB signal
CC sequence and ScFvOxazon. This sequence was used in the method of the
CC present invention
XX
SQ Sequence 255 AA;

Query Match 73.3%; Score 444; DB 4; Length 255;
Best Local Similarity 80.0%; Pred. No. 4.2e-27;
Matches 88; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTMTCSASSSVNYMHWFQESGTFPPKRRYDTSKLASGVPAR 60
Db |||||
132 DIELTQSPAIMASPGKVTMTCSASSSVRYMNVWFQKSGTSPKRWIYDTSKLSSGVPAR 191

QY 61 LSGSGSGTEFTLEISRVAEDVGYYCQQLVEYPLTFGAGTKLELKRADA 110
Db ||||| :|| :|||
192 FSGSGSGTSLTSSMEABDAATYYCQQWSSNPLTFGAGTKLELKRAAA 241

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Job time : 115.067 secs

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OM protein - protein search, using sw model

Run on: October 13, 2004, 12:59:19 ; Search time 85.7792 Seconds
(without alignments)
447.653 Million cell updates/sec

Title: US-10-049-860A-3
Perfect score: 606
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1356558 seqs, 322682953 residues

Total number of hits satisfying chosen parameters:	1356558
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Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Published Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	471	77.7	215	14	US-10-410-907A-34	Sequence 34, Appl
2	459	75.7	129	14	US-10-344-779-2	Sequence 2, Appli
3	459	75.7	129	16	US-10-738-809-2	Sequence 2, Appli
4	458	75.6	235	9	US-09-910-059-17	Sequence 17, Appl
5	452	74.6	108	16	US-10-803-622-251	Sequence 251, App
6	452	74.6	108	16	US-10-803-653-251	Sequence 251, App
7	448	73.9	108	16	US-10-803-622-243	Sequence 243, App
8	448	73.9	108	16	US-10-803-653-243	Sequence 243, App
9	446	73.6	108	16	US-10-803-622-241	Sequence 241, App
10	446	73.6	108	16	US-10-803-653-241	Sequence 241, App
11	445	73.4	235	10	US-09-795-515-5	Sequence 5, Appli
12	445	73.4	235	15	US-10-704-352-5	Sequence 5, Appli
13	445	73.4	235	15	US-10-704-071-5	Sequence 5, Appli
14	440	72.6	107	9	US-09-144-886-82	Sequence 82, Appl

ALIGNMENTS

RESULT 1

US-10-410-907A-34

```

; Sequence 34, Application US/10410907A
; Publication No. US20030215880A1
; GENERAL INFORMATION:
; APPLICANT: Dennis R. Burton
; APPLICANT: R. Anthony Williamson
; APPLICANT: Gianluca Moroncini
; TITLE OF INVENTION: MOTIF-GRAFTED HYBRID POLYPEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 22908-1229
; CURRENT APPLICATION NUMBER: US/10/410,907A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/371,610
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
;   LENGTH: 215
;   TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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OTHER INFORMATION: D18 Light Chain
US-10-410-907A-34

Query Match 77.7%; Score 471; DB 14; Length 215;
Best Local Similarity 77.8%; Pred. No. 7.3e-36;
Matches 91; Conservative 9; Mismatches 17; Indels

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D b	3	E	L	V	L	T	Q	S	P	A	F	M	S	A	S	P	G	E	K	V	T	M	T	C	S	A	S	S	S	V	N	M	H	W	Y	Q	O	K	S	G	T	S	P	K	R	W	I	Y	D	T	S	K	L	A	S	G	V	P	A	R	62
QY	61	L	S	G	S	G	T	E	F	T	L	E	I	S	R	V	K	A	E	D	V	G	V	Y	C	Q	L	V	E	Y	P	L	T	F	G	A	G	T	K	L	E	L	K	R	A	D	A	P	T	V	S	I	F	117							
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```
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,622
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 251
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-251

Query Match          74.6%; Score 452; DB 16; Length 108;
Best Local Similarity 81.5%; Pred. No. 2e-34;
Matches 88; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTMTCSASSSVNYMHWFQQESGTFPKRRIYDTSKLAGVVPAR 60
Db 1 DIELTQSPAIMASPGKVTMTCSASSSVNYMHWFQQESGTFPKRRIYDTSKLAGVVPAR 60

QY 61 LSGSGSGTEFTLEISRVAEDVGYYCQQLVVEPLTFGAGTKLEIKRA 108
Db 61 FSGSGSGTSYSLTSSMEAEADVATYYCQQWSSNPLTFGAGTKLEIKRA 108

RESULT 6
US-10-803-653-251
; Sequence 251, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,653
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
```

```
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 251
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-251

Query Match          74.6%; Score 452; DB 16; Length 108;
Best Local Similarity 81.5%; Pred. No. 2e-34;
Matches 88; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTMTCSASSSVNYMHWFQQESGTFPKRRIYDTSKLAGVVPAR 60
Db 1 DIELTQSPAIMASPGKVTMTCSASSSVNYMHWFQQESGTFPKRRIYDTSKLAGVVPAR 60

QY 61 LSGSGSGTEFTLEISRVAEDVGYYCQQLVVEPLTFGAGTKLEIKRA 108
Db 61 FSGSGSGTSYSLTSSMEAEADVATYYCQQWSSNPLTFGAGTKLEIKRA 108

RESULT 7
US-10-803-622-243
; Sequence 243, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,622
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
```

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; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 243
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-243

Query Match      73.9%; Score 448; DB 16; Length 108;
Best Local Similarity 80.6%; Pred. No. 4.7e-34;
Matches 87; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY      1 DIELTQSPAIMSASPGEKVTMTCSASSSVNVMHWFQQESGTFPKRRIYDTSKLAGVPAR 60
      |||||
Db      1 DIELTQSPAIMSASPGEKVTMTCSASSSVNVMHWFQQESGTFPKRRIYDTSKLAGVPAR 60
      |||||

QY      61 LSGSGSGTEFTLEISRKAEVDGVVYCCQLVEYPLTFGAGTKLEIKRA 108
      |||||:::|||||
Db      61 FSGSGSGTSYSLTSSMEAEADAATYYCQWSSNPLTFGAGTKLEIKRA 108
      |||||:::|||||

RESULT 8
US-10-803-653-243
; Sequence 243, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,653
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR APPLICATION NUMBER: US 08/484,893
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; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 243
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-243

Query Match      73.9%; Score 448; DB 16; Length 108;
Best Local Similarity 80.6%; Pred. No. 4.7e-34;
Matches 87; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY      1 DIELTQSPAIMSASPGEKVTMTCSASSSVNVMHWFQQESGTFPKRRIYDTSKLAGVPAR 60
      |||||
Db      1 DIELTQSPAIMSASPGEKVTMTCSASSSVNVMHWFQQESGTFPKRRIYDTSKLAGVPAR 60
      |||||

QY      61 LSGSGSGTEFTLEISRKAEVDGVVYCCQLVEYPLTFGAGTKLEIKRA 108
      |||||:::|||||
Db      61 FSGSGSGTSYSLTSSMEAEADAATYYCQWSSNPLTFGAGTKLEIKRA 108
      |||||:::|||||

RESULT 9
US-10-803-622-241
; Sequence 241, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,622
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-241

Query Match 73.6%; Score 446; DB 16; Length 108;
Best Local Similarity 80.6%; Pred. No. 7.2e-34;
Matches 87; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTMTCSASSSVNYMHWFQOESGTFPKRRIYDTSKLAGVGP 60
Db 1 DIELTQSPAIMASPGKVTMTCSASSSVNYMHWFQOESGTFPKRRIYDTSKLAGVGP 60
QY 61 LSGSGSGTEFTLEISRVAEDVGYYCQQLVEYPLTFGAGTKLELKRA 108
Db 61 FSGSGSGTSYSLTISSMEADAATYYCQFSSNPLTFGAGTKLELKRA 108

RESULT 10
US-10-803-653-241
Sequence 241, Application US/10803653
Publication No. US20040157215A1
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clarkson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 13839-00013
CURRENT APPLICATION NUMBER: US/10/803,653
CURRENT FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 241
LENGTH: 108
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-241

Query Match 73.6%; Score 446; DB 16; Length 108;
Best Local Similarity 80.6%; Pred. No. 7.2e-34;
Matches 87; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMASPGKVTMTCSASSSVNYMHWFQOESGTFPKRRIYDTSKLAGVGP 60

Db 1 DIELTQSPAIMASPGKVTMTCSASSSVNYMHWFQOESGTFPKRRIYDTSKLAGVGP 60
QY 61 LSGSGSGTEFTLEISRVAEDVGYYCQQLVEYPLTFGAGTKLELKRA 108
Db 61 FSGSGSGTSYSLTISSMEADAATYYCQFSSNPLTFGAGTKLELKRA 108

RESULT 11
US-09-795-515-5
Sequence 5, Application US/09795515
Publication No. US20030039645A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-795-515-5

Query Match 73.4%; Score 445; DB 10; Length 235;
Best Local Similarity 75.0%; Pred. No. 2.1e-33;
Matches 87; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 2 IELTQSPAIMASPGKVTMTCSASSSVNYMHWFQOESGTFPKRRIYDTSKLAGVGP 61
Db 24 IVLTQSPAIMASPGKVTMTCSASSSVNYMHWFQOESGTFPKRRIYDTSKLAGVPAHF 83
QY 62 SGSGSGTEFTLEISRVAEDVGYYCQQLVEYPLTFGAGTKLELKRAAAPTVSIF 117
Db 84 RSGSGSGTSYSLTISSMEADAATYYCQWSSNPFTFGSGTKLEINRADTAPTVSIF 139

RESULT 12
US-10-704-352-5
Sequence 5, Application US/10704352
Publication No. US20040071693A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
Athwal, Diljeet S.
Emtage, John S.


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RESULT 15
US-09-144-886-83
; Sequence 83, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone
; OTHER INFORMATION: IG7 region VL epitope 1
US-09-144-886-83

Query Match      72.6%; Score 440; DB 9; Length 107;
Best Local Similarity 80.4%; Pred. No. 2.6e-33;
Matches 86; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY      1 DIELTQSPAIMSASPGEKVTMTCSASSSVNYMHWFOQESGTFPKRRIYDTSKLAGVYPAR 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 DIELTQSPAIMSASPGEKVTMTCSASSSVNYMHWYQQKSGTSPKRWIYDTSKLAGVYPAR 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY      61 LSGSGSGTEFTLEISRVKAEVDGVVYQCQLVEYPLTFGAGTKLELKR 107
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 FSGSGSGTSYSLTISSEMEADAATYYCQOWSSNPLTFGAGTKLELKR 107
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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Search completed: October 13, 2004, 13:15:27
Job time : 86.7792 secs

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OM protein - protein search, using sw model

Run on: October 13, 2004, 12:48:23 ; Search time 24.7042 Seconds
(without alignments)
471.266 Million cell updates/sec

Title: US-10-049-868A-4
Perfect score: 635
Sequence: 1 QVQLQESGPGLVAPQSLSI.....MITAYAMDYWGQTTVTSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	552.5	87.0	141	2	S52446	Ig heavy chain V r
2	536	84.4	112	2	S11100	Ig heavy chain V r
3	533.5	84.0	117	2	S38563	Ig heavy chain V r
4	530.5	83.5	120	2	PL0087	Ig heavy chain V r
5	529	83.3	140	2	S55028	Ig heavy chain V r
6	527	83.0	113	2	S11101	Ig heavy chain V r
7	527	83.0	114	2	S11106	Ig heavy chain V r
8	527	83.0	116	2	S11102	Ig heavy chain V r
9	524.5	82.6	139	2	A32456	Ig heavy chain pre
10	521	82.0	112	2	S11108	Ig heavy chain V r
11	517	81.4	115	2	S11103	Ig heavy chain V r
12	515	81.1	114	2	S11099	Ig heavy chain V r
13	507.5	79.9	116	2	S42484	Ig heavy chain V r
14	500.5	78.8	122	2	A49049	Ig heavy chain V r
15	500	78.7	106	2	S26322	Ig heavy chain V r
16	499	78.6	118	2	PQ0266	Ig heavy chain V r
17	497.5	78.3	135	2	S31913	Ig heavy chain V r
18	492.5	77.6	122	2	S20809	Ig gamma-2A chain
19	492	77.5	106	2	S14489	Ig heavy chain V r
20	492	77.5	114	2	S11105	Ig heavy chain V r
21	491	77.3	112	2	S11098	Ig heavy chain V r
22	490	77.2	117	2	S10111	Ig heavy chain V r
23	489	77.0	140	2	S14238	Ig gamma-1 chain p
24	487	76.7	127	2	B31807	Ig heavy chain V r
25	487	76.7	144	1	G2MS14	Ig heavy chain pre
26	486.5	76.6	118	2	S32786	Ig heavy chain (an
27	483	76.1	121	2	D30560	Ig heavy chain V r
28	480	75.6	121	2	S33131	Ig heavy chain V r
29	480	75.6	231	2	PC4155	Ig gamma-2b chain

30	479	75.4	109	2	S11109	Ig heavy chain V r
31	479	75.4	114	2	S11104	Ig heavy chain V r
32	478.5	75.4	144	2	S11244	Ig gamma-2a chain
33	477	75.1	107	2	S14492	Ig heavy chain V r
34	476	75.0	107	2	S14493	Ig heavy chain V r
35	475	74.8	100	2	S14490	Ig heavy chain V r
36	473	74.5	115	2	S11107	Ig heavy chain V r
37	471	74.2	111	2	S26324	Ig heavy chain V r
38	471	74.2	114	2	S26321	Ig heavy chain V r
39	470	74.0	107	2	S14491	Ig heavy chain V r
40	467.5	73.6	110	2	PH1024	Ig heavy chain V r
41	467	73.5	95	2	S17605	Ig heavy chain V r
42	464	73.1	110	2	S26323	Ig heavy chain V r
43	463	72.9	109	2	PH1025	Ig heavy chain V r
44	461.5	72.7	115	2	S26470	Ig heavy chain V r
45	455	71.7	101	2	S03466	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S52446
Ig heavy chain V region precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 03-Aug-1995 #text_change 23-Jul-1999
C;Accession: S52446
R;Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of rearranged ge
A;Reference number: S52445
A;Accession: S52446
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-141 <BER>
A;Cross-references: EMBL:X82692; NID:g673441; PIDN:CAA58013.1; PID:g673442
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match	87.0%;	Score	552.5;	DB	2;	Length	141;
Best Local Similarity	89.3%;	Pred.	No. 3.1e-45;				
Matches	109;	Conservative	2;	Mismatches	10;	Indels	1;
Gaps	1;						
QY	1	QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLVITGGSNTYN	60				
Db	20	QVQLKESGPGLVAPQSLSITCTVSGFSLTSYGVHVRQPPGKGLGVITAGGSNTYN	79				
QY	61	SALMSRLSISKDNSKSKQVFLKMNLSQTDVTDYMYCARD-RSTMITAYAMDYWGQTTVTV	119				
Db	80	SALMSRLSISKDNSKSKQVFLKMNLSQIDDTAMYYCARSPSTMTDTPYANDYWGQTSVTV	139				
QY	120	SS 121					
Db	140	SS 141					

RESULT 2
S11100
Ig heavy chain V region (clone NQ2-20.5.3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C;Accession: S11100
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A;Reference number: S07331; MUID:83271467; PMID:6877353
A;Accession: S11100
A;Molecule type: mRNA
A;Residues: 1-112 <NAT>
C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 84.4%; Score 536; DB 2; Length 112;
Best Local Similarity 86.7%; Pred. No. 8.7e-44;
Matches 104; Conservative 1; Mismatches 7; Indels 8; Gaps 1;

QY 1 QVQLQESGPGLVAPSQSLSTCTVSGISLNRYGVHWRQPPGKGLEWLGVIWTGGSTNYN 60
||||:|||||
Db 1 QVQLKESGPGLVAPSQSLSTCTVSGXSLTSYGVHWRQPPGKGLEWLGVIWAGGSTNYN 60
||||:|||||

QY 61 SALMSRLSISKDNSKSKQVFLKMNSLQTDTTAMYYCARDRSTMITAYAMDYWGQTTVTVS 120
||||:|||||
Db 61 SALMSRLSISKDNSKSKQVFLKMNSLQTDTTAMYYCARDRGX-----YWGQGLTVTVS 112
||||:|||||

RESULT 3

S38563
Ig heavy chain V region (ASWS1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38563
R;Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
submitted to the EMBL Data Library, September 1993
A;Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2s M
A;Reference number: S38559
A;Accession: S38563
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <MON>
A;Cross-references: EMBL:X75099; NID:G414151; PIDN:CAA52990.1; PID:G414152
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 533.5; DB 2; Length 117;
Best Local Similarity 85.8%; Pred. No. 1.6e-43;
Matches 103; Conservative 6; Mismatches 8; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVAPSQSLSTCTVSGISLNRYGVHWRQPPGKGLEWLGVIWTGGSTNYN 60
||||:|||||
Db 1 QVQLKESGPGLVAPSQSLSTCTVSGFSLRSYSHWRQPPGKGLEWLGMIWGGNTDYN 60
||||:|||||

QY 61 SALMSRLSISKDNSKSKQVFLKMNSLQTDTTAMYYCARDRSTMITAYAMDYWGQTTVTVS 120
||||:|||||
Db 61 SALKSRLSISKDNSKSKQVFLKMNSLQTDTTAMYYCARDG--YYDYAMDYWGQTSVTVS 117
||||:|||||

RESULT 4

PL0087
Ig heavy chain V region (E3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PL0087
R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca
J. Exp. Med. 169, 519-533, 1989
A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are
A;Reference number: PL0080; MUID:89094248; PMID:2492056
A;Accession: PL0087
A;Molecule type: mRNA
A;Residues: 1-120 <MEE>
A;Cross-references: GB:X58593; GB:Y00794; NID:G51571; PIDN:CAA41468.1; PID:G938252
A;Experimental source: strain BALB/c
A;Note: the sequence shown here is from the VH region of an antiidiotypic monoclonal ant
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 83.5%; Score 530.5; DB 2; Length 120;
Best Local Similarity 86.0%; Pred. No. 3.1e-43;
Matches 104; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

QY 1 QVQLQESGPGLVAPSQSLSTCTVSGISLNRYGVHWRQPPGKGLEWLGVIWTGGSTNYN 60
||||:|||||

Db 1 QVQLKRSRGPGLVAPSQSLSTCTVSGFSLTSSGVHWRQPPGKGLEWLGVIWAGGSTNYN 60
||||:|||||

QY 61 SALMSRLSISKDNSKSKQVFLKMNSLQTDTTAMYYCARDRSTMITAYAMDYWGQTTVTVS 120
||||:|||||

Db 61 SALMSRLTISKDNSKSKQVFLKMNTSLQIDTTAMYYCARD-SHCGQAYGMDYWGQTSVTVS 119
||||:|||||

QY 121 S 121
|
Db 120 S 120
|

RESULT 5

S55028
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 23-Jul-1999
C;Accession: S55028
R;Jeffrey, P.D.; Schildbach, J.F.; Chang, C.Y.; Kussie, P.H.; Margolies, M.N.; Sheriff,
J. Mol. Biol. 248, 344-360, 1995
A;Title: Structure and specificity of the anti-digoxin antibody 40-50.
A;Reference number: S55027; MUID:95257394; PMID:7739045
A;Accession: S55028
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <JEF>
A;Cross-references: EMBL:L31403; NID:G476717; PIDN:AAA38191.1; PID:G476718
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 83.3%; Score 529; DB 2; Length 140;
Best Local Similarity 82.6%; Pred. No. 5.1e-43;
Matches 100; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVAPSQSLSTCTVSGISLNRYGVHWRQPPGKGLEWLGVIWTGGSTNYN 60
||||:|||||

Db 20 QVHLKESGPGLVAPSQSLSTCTVSGFSLTTYGVHWRQPPGKGLEWLGLIWAGNTDYN 79
||||:|||||

QY 61 SALMSRLSISKDNSKSKQVFLKMNSLQTDTTAMYYCARDRSTMITAYAMDYWGQTTVTVS 120
||||:|||||

Db 80 SALMSRLSINKDNSKSKQVFLKMNSLQADTTAMYYCARFRFASYDYAVDYWGQTSVTVS 139
||||:|||||

QY 121 S 121
|
Db 140 S 140
|

RESULT 6

S11101
Ig heavy chain V region (clone NQ2-48.2.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C;Accession: S11101
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazol
A;Reference number: S07331; MUID:83271467; PMID:6877353
A;Accession: S11101
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <KAA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 527; DB 2; Length 113;
Best Local Similarity 84.3%; Pred. No. 6.2e-43;
Matches 102; Conservative 2; Mismatches 9; Indels 8; Gaps 1;

QY 1 QVQLQESGPGLVAPSQSLSTCTVSGISLNRYGVHWRQPPGKGLEWLGVIWTGGSTNYN 60
||||:|||||

Db 1 QVQLKESGPGLVXPSQSLSTCTVSGXSLTSYGVHWRQPPGKGLEWLGVIWAGGSTNYN 60
||||:|||||

QY 61 SALMSRLSISKDNSKSKQVFLKMNSLQTDTTAMYYCARDRSTMITAYAMDYWGQTTVTVS 120
||||:|||||

```
Db      ||||||| 61 SALMSRLSISKDNSKSVFLKMNLSQTDDTAMYYCARDRGV-----YWGQGLTVTVS 112
QY      121 S 121
Db      113 A 113

RESULT 7
S11106
Ig heavy chain V region (clone NQ5-96.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C;Accession: S11106
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A;Reference number: S07331; MUID:83271467; PMID:6877353
A;Accession: S11106
A;Molecule type: mRNA
A;Residues: 1-114 <NAT>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match      83.0%; Score 527; DB 2; Length 114;
Best Local Similarity 84.3%; Pred. No. 6.3e-43;
Matches 102; Conservative 2; Mismatches 9; Indels 8; Gaps 1;

QY      1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWTGGSTNYN 60
Db      |||||:||||| 1 QVQLKEXGPGLVXPSQSLITCTVSGXSLTSYGVHVRQPPGKGLEWLGVIWAGGSINYN 60
QY      61 SALMSRLSISKDNSKSQVFLKMNLSQTDDTAMYYCARDRSTMITAYAMDYWGQGTITVTVS 120
Db      ||||||| 61 SALMSRLSISKDNSKSQVFLKMNLSQTDDTAMYYCARD-----GFAYWGQGTITVTVS 112
QY      121 S 121
Db      113 S 113

RESULT 8
S11102
Ig heavy chain V region (clone NQ5-4.3.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C;Accession: S11102
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A;Reference number: S07331; MUID:83271467; PMID:6877353
A;Accession: S11102
A;Molecule type: mRNA
A;Residues: 1-116 <NAT>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match      83.0%; Score 527; DB 2; Length 116;
Best Local Similarity 84.3%; Pred. No. 6.4e-43;
Matches 102; Conservative 2; Mismatches 9; Indels 8; Gaps 1;

QY      1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWTGGSTNYN 60
Db      ||||||| 1 QVQLKEXGPGLVXPSQSLITCTVSGXSLTSYGVHVRQPPGKGLEWLGVIWAGGSINYN 60
QY      61 SALMSRLSISKDNSKSQVFLKMNLSQTDDTAMYYCARDRSTMITAYAMDYWGQGTITVTVS 120
Db      ||||||| 61 SALMSRLSISKDNSKSVFLKMNLSQTDDTAMYYCARDGX-----YWGQGLTVTVS 112
QY      121 S 121
Db      113 A 113
```

```
RESULT 9
A32456
Ig heavy chain precursor V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999
C;Accession: A32456
R;Dombrink-Kurtzman, M.A.; Johnson, L.S.; Riordan, G.S.; Bedzyk, W.D.; Voss Jr., E.W.
J. Biol. Chem. 264, 4513-4522, 1989
A;Title: Variable region primary structures of a high affinity anti-fluorescein immunoglobulin
A;Reference number: A32456; MUID:89174706; PMID:2494173
A;Accession: A32456
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-139 <DOM>
A;Cross-references: GB:J04609; NID:G556316; PIDN:AAA50298.1; PID:G556317
A;Note: the authors translated the codon CAC for residue 20 as Gln, and CAC for residue
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match      82.6%; Score 524.5; DB 2; Length 139;
Best Local Similarity 85.0%; Pred. No. 1.3e-42;
Matches 102; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY      2 VQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWTGGSTNYNS 61
Db      |||||:||||| 21 VHLKESGPGVLVAPSQSLITCTVSGFSLTNYGVHVRQPPGKGLEWLGVIWAGGNTNYNS 80
QY      62 ALMSRLSISKDNSKSQVFLKMNLSQTDDTAMYYCARDRSTMITAYAMDYWGQGTITVTVSS 121
Db      ||||||| 81 ALMSRLSISKDNSKSQVFLKMNLSQIDDTAIYYCAK-RLERIFYAMDYWGQGTITVTVSS 139

RESULT 10
S11108
Ig heavy chain V region (clone NQ5-78.2.6) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C;Accession: S11108
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A;Reference number: S07331; MUID:83271467; PMID:6877353
A;Accession: S11108
A;Molecule type: mRNA
A;Residues: 1-112 <NAT>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match      82.0%; Score 521; DB 2; Length 112;
Best Local Similarity 84.2%; Pred. No. 2.3e-42;
Matches 101; Conservative 2; Mismatches 9; Indels 8; Gaps 1;

QY      1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWTGGSTNYN 60
Db      |||||:||||| 1 QVQLKESGPGLVXPSQSLITCTVSGXSLTSYGVHVRQPPGKGLEWLGVIWAGGNTNYN 60
QY      61 SALMSRLSISKDNSKSQVFLKMNLSQTDDTAMYYCARDRSTMITAYAMDYWGQGTITVTVS 120
Db      ||||||| 61 SALMSRLSISKDNSKSQVFXKMNSLQTDTTAMYYXCARDRE-----DYWGXGTSVTVS 112

RESULT 11
S11103
Ig heavy chain V region (clone NQ5-61.1.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C;Accession: S11103
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A;Reference number: S07331; MUID:83271467; PMID:6877353
```


A;Accession: S11103
A;Molecule type: mRNA
A;Residues: 1-115 <NAT>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 517; DB 2; Length 115;
Best Local Similarity 83.5%; Pred. No. 5.6e-42;
Matches 101; Conservative 2; Mismatches 10; Indels 8; Gaps 1;

QY 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWGGSTNYN 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLKESGPGLVAPSQSLITCTVSGXSLTSXGVHVRQPPGKGLEWLGVIWAGGSTNYN 60

QY 61 SALMSRLSISKDNSKSKVFLKMNLSLQTDTTAMYCARDSTMITAYAMDYWGQGTITVTS 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SALMSRLSISKDNSKSKVFLKMNLSLQTDTTAMYCARDRGA-----YWGXTLTVTS 112

QY 121 S 121
:
Db 113 A 113

RESULT 12
S11099
Ig heavy chain V region (clone NQ2-17.4.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C;Accession: S11099
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A;Reference number: S07331; MUID:83271467; PMID:6877353
A;Accession: S11099
A;Molecule type: mRNA
A;Residues: 1-114 <NAT>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 81.1%; Score 515; DB 2; Length 114;
Best Local Similarity 82.6%; Pred. No. 8.6e-42;
Matches 100; Conservative 2; Mismatches 11; Indels 8; Gaps 1;

QY 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWGGSTNYN 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLKESGPGLVAPSQSLITCTVSGXSLTSYGVHVRQPPGKGLEWLGVIWAGGSTNYN 60

QY 61 SALMSRLSISKDNSKSKVFLKMNLSLQTDTTAMYCARDSTMITAYAMDYWGQGTITVTS 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SALMSRLSISKDNSKSKVFLKMNLSLQTDTTAMYCARDXGA-----YWGQGLTXTS 112

QY 121 S 121
:
Db 113 A 113

RESULT 13
S42484
Ig heavy chain V region (4B1 VH) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
C;Accession: S42484
R;Gilbert, D.; Brard, F.; Margairitte, C.; Delpech, A.; Tron, F.
submitted to the EMBL Data Library, March 1994
A;Description: An idiotype D23-bearing polyspecific, murine anti-DNA monoclonal antibody
A;Reference number: S42484
A;Accession: S42484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <GIL>
A;Cross-references: EMBL:Z30962; NID:g461325; PIDN:CAA83216.1; PID:g461326
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 79.9%; Score 507.5; DB 2; Length 116;
Best Local Similarity 80.3%; Pred. No. 4.5e-41;
Matches 98; Conservative 6; Mismatches 11; Indels 7; Gaps 2;

QY 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWGGSTNYN 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLQESGPGLVAPSQSLITCTVSGFSLTSYAISWVRQPPGKGLEWLGVIWGGSTNYN 60

QY 61 SALMSRLSISKDNSKSKVFLKMNLSLQTDTTAMYCARDSTMITAYA-MDYWGQGTITV 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SALKSRLSISKDNSKSKIFLKLNSLQTDAAARYFCARD-----GYSFFDYWGQGTTLTV 114

QY 120 SS 121
||
Db 115 SS 116

RESULT 14
A49049
Ig heavy chain V region (anti-idiotypic) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
C;Accession: A49049
R;Armandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.
Eur. J. Immunol. 22, 2893-2899, 1992
A;Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR antigenic determinant
A;Reference number: A49049; MUID:93049629; PMID:1425914
A;Accession: A49049
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-122 <ARM>
A;Experimental source: BALB/c
A;Note: sequence extracted from NCBI backbone (NCBIN:118295, NCBIIP:118296)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 500.5; DB 2; Length 122;
Best Local Similarity 81.8%; Pred. No. 2.2e-40;
Matches 99; Conservative 6; Mismatches 13; Indels 3; Gaps 2;

QY 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWGGSTNYN 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLKESGPGLVAPSQSLITCTVSGFSITDYVVSWIRQPPGKGLEWLGVIWGGSTNYN 60

QY 61 SALMSRLSISKDNSKSKVFLKMNLSLQTDTTAMYCARDSTMITAYAMDYWGQGTITVTS 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SALKSRLSISKDNSKSKVFLKMNLSLQTDTTAMYCAKHEDE--ITTY-FDYWGQGTTLTVS 117

QY 121 S 121
|
Db 118 S 118

RESULT 15
S26322
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C;Accession: S26322
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26322
A;Molecule type: mRNA
A;Residues: 1-106 <STA>
A;Cross-references: EMBL:X59182
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-91/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 500; DB 2; Length 106;
Best Local Similarity 85.1%; Pred. No. 2.1e-40;
Matches 97; Conservative 2; Mismatches 7; Indels 8; Gaps 1;
QY 7 SGPGLVAPSQSL SITCTVSGISLNRVGVHVRQPPGKGLEWLGVIWTGGSTNYSALMSR 66
Db 1 SGPGLVAPSQSL SITCTVSGISLNRVGVHVRQPPGKGLEWLGVIWTGGSTNYSALMSR 60
QY 67 LSISKDNSKQVFLKMNSLQTD TDTAMYICARDRSTMITAYAMDYWGQGT TVTVS 120
Db 61 LSISKDNSKQVFLKMNSLQTD TDTAMYICARE-----ALRLWGQGT LVTVS 106

Search completed: October 13, 2004, 13:00:06
Job time : 24.7042 secs

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OM protein - protein search, using sw model

Run on: October 13, 2004, 12:47:33 ; Search time 121 Seconds
(without alignments)
575.375 Million cell updates/sec

Title: US-10-049-868A-4
Perfect score: 635
Sequence: 1 QVQLQESGPGLVAPQSLSI.....MITAYAMDYWGQTTVTSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	506.5	79.8	482	2 Q91X92	Q91x92 mus musculus
2	490.5	77.2	121	2 Q99NG4	Q99ng4 mus musculus
3	487	76.7	144	1 HV43_MOUSE	P01819 mus musculus
4	442	69.6	115	1 HV44_MOUSE	P01820 mus musculus
5	436	68.7	116	1 HV45_MOUSE	P01821 mus musculus
6	401.5	63.2	135	1 HV02_XENLA	P20957 xenopus lae
7	389.5	61.3	465	2 Q6GMX6	Q6gmxx6 homo sapien
8	382	60.2	129	2 BAD00255	Bad00255 camelus d
9	376	59.2	119	2 Q9UL73	Q9ul73 homo sapien
10	373	58.7	121	1 HV3J_HUMAN	P01771 homo sapien
11	371.5	58.5	620	2 Q96EY0	Q96ey0 homo sapien
12	366	57.6	476	2 Q6GMX1	Q6gmxx1 homo sapien
13	364.5	57.4	477	2 Q6GMX7	Q6gmxx7 homo sapien
14	364.5	57.4	576	2 Q6P4I8	Q6p4i8 homo sapien
15	364.5	57.4	576	2 AAH63384	Aah63384 homo sapi
16	364	57.3	137	1 HV46_MOUSE	P01822 mus musculus
17	361.5	56.9	124	2 BAD00233	Bad00233 camelus d
18	358.5	56.5	478	2 Q7Z379	Q7z379 homo sapien
19	356.5	56.1	573	2 Q8WU38	Q8wu38 homo sapien
20	355	55.9	483	2 BAC85202	Bac85202 homo sapien
21	354	55.7	595	2 Q8WUX4	Q8wux4 homo sapien
22	354	55.7	597	2 Q6GMX5	Q6gmxx5 homo sapien
23	354	55.7	597	2 Q9BU10	Q9bul0 homo sapien
24	354	55.7	625	2 Q96AA6	Q96aa6 homo sapien
25	353.5	55.7	112	2 Q9HCC1	Q9hcc1 homo sapien
26	353	55.6	499	2 Q8N5K4	Q8n5k4 homo sapien
27	352	55.4	472	2 Q6N089	Q6n089 homo sapien
28	352	55.4	472	2 CAE45781	Cae45781 homo sapi
29	352	55.4	501	2 BAC85359	Bac85359 homo sapi
30	351	55.3	136	1 HV01_XENLA	P20956 xenopus lae
31	350	55.1	120	2 BAD00465	Bad00465 camelus d

32	350	55.1	128	2 BAD00406	Bad00406 camelus d
33	348.5	54.9	122	1 HV3G_HUMAN	P01768 homo sapien
34	348	54.8	597	2 Q9BQ58	Q9bqb8 homo sapien
35	347	54.6	479	2 BAC85434	Bac85434 homo sapi
36	346	54.5	470	2 BAC85387	Bac85387 homo sapi
37	345.5	54.4	118	2 Q811U5	Q81lu5 mus musculu
38	344.5	54.3	613	2 Q8WUK1	Q8wuk1 homo sapien
39	343	54.0	139	2 Q86SX2	Q86sx2 homo sapien
40	342.5	53.9	120	2 AAL35864	Aal35864 lama glam
41	341.5	53.8	136	2 Q6LBQ5	Q6lbq5 mus musculu
42	341.5	53.8	136	2 CAA34714	Caa34714 mus muscu
43	341	53.7	472	2 BAC85393	Bac85393 homo sapi
44	340	53.5	254	2 BAC86524	Bac86524 homo sapi
45	339.5	53.5	494	2 BAC85198	Bac85198 homo sapi

ALIGNMENTS

RESULT 1
Q91X92

ID	Q91X92	PRELIMINARY;	PRT;	482 AA.
AC	Q91X92;			
DT	01-DEC-2001 (Tremblrel. 19, Created)			
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Igh-VJ558 protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FVB/N; TISSUE=Colon;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FVB/N; TISSUE=Colon;			
RA	Strausberg R.;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC011181; AAH11181.1; -.			
DR	PIR; F33932; F33932.			
DR	HSSP; P01820; 1A7N.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig_c1.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF07654; Cl-set; 2.			
DR	Pfam; PF00047; ig; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 4.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN 2.			
SQ	SEQUENCE 482 AA; 51864 MW; 312E01F9C1BC7F3C CRC64;			

Query Match		79.8%;	Score 506.5;	DB 2;	Length 482;
Best Local Similarity		81.3%;	Pred. No. 2.2e-44;		
Matches 100;		Conservative 6;	Mismatches 10;	Indels 7;	Gaps 2;
QY	1	QVQLQESGPGLVAPSQSL	ITCTVSGISLNRYGVHWVRQPPGKGL	EWLGV	IWTGGSTNYN 60
Db	20	QVQLKESGPDVAPSQSL	ITCTVSGFALTSAISWVRQPPGKGL	EWLGV	IWTGGVTNYN 79
QY	61	SALMSRLSISKDN	SKSQVFLKMNSLQTD	DTAMYYCARDRSTMITAY--	AMDYWGQTTVT 118
Db	80	SALKSRLSISKDN	SKSQVFLKMNSLQTD	TARYYCARDSN-----	YEGAMDYWGQGTSTVT 134
QY	119	VSS	121		
Db	135	VSS	137		
RESULT 2					
Q99NG4	ID	Q99NG4	PRELIMINARY;	PRT;	121 AA.
AC	Q99NG4;				
DT	01-JUN-2001	(TrEMBLrel. 17, Created)			
DT	01-JUN-2001	(TrEMBLrel. 17, Last sequence update)			
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)			
DE	Single chain Fv (Fragment).				
OS	Mus musculus (Mouse).				
OG	Plasmid PHEN1.				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BALB/C;				
RX	MEDLINE=98169018; PubMed=9510199;				
RA	Hawlich H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L.,				
RA	Bautsch W., Kola A., Klos A., Koehl J.;				
RT	"Site-Directed C3a-Receptor Antibodies from Phage Display Libraries.";				
RL	J. Immunol. 160:2947-2958(1998).				
DR	EMBL; AJ222590; CAA10890.1; -.				
DR	PIR; F33932; F33932.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; ig; 1.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
KW	Plasmid.				
FT	NON_TER 1				
FT	NON_TER 121				
SQ	SEQUENCE 121 AA; 13255 MW; D293E4EBC8C59D5B CRC64;				
Query Match		77.2%;	Score 490.5;	DB 2;	Length 121;
Best Local Similarity		79.3%;	Pred. No. 2e-43;		
Matches 96;		Conservative 8;	Mismatches 16;	Indels 1;	Gaps 1;
QY	1	QVQLQESGPGLVAPSQSL	ITCTVSGISLNRYGVHWVRQPPGKGL	EWLGV	IWTGGSTNYN 60
Db	1	QVQLKESGPGLVAPSQSL	ITCTVSGFPLTSHGVSWVRQPPGKGL	EWLGV	IWGDGNTKYH 60
QY	61	SALMSRLSISKDN	SKSQVFLKMNSLQTD	DTAMYYCARDRSTMITAY	AMDYWGQTTVTS 120
Db	61	SALISRLSISKDN	SKSQVFLKLNLSQTD	TATYYCAR-HYYKYANY	AMDYWGQGTSTVTS 119
QY	121	S	121		
Db	120	S	120		
RESULT 3					
ID	HV43_MOUSE				
ID	HV43_MOUSE	STANDARD;	PRT;	144	AA.
AC	P01819;				
DT	21-JUL-1986 (Rel. 01, Created)				

DT	21-JUL-1986	(Rel. 01, Last sequence update)			
DT	29-MAR-2004	(Rel. 43, Last annotation update)			
DE	Ig heavy chain V region MOPC 141 precursor.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=81012133; PubMed=6774258;				
RA	Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;				
RT	"Two types of somatic recombination are necessary for the generation of complete immunoglobulin heavy-chain genes.";				
RL	Nature 286:676-683(1980).				
CC	-!- MISCELLANEOUS: The sequence shown is translated from a				
CC	differentiated gene isolated from a myeloma that secretes IgG2b.				
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like domain.				
CC	-----				
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CC	-----				
DR	EMBL; J00491;	AAA38121.1;	-.		
DR	PIR; A02094;	G2MS14.			
DR	HSSP; P01820;	1G7J.			
DR	InterPro; IPR007110;	Ig-like.			
DR	InterPro; IPR003596;	Ig_v.			
DR	Pfam; PF00047;	ig; 1.			
DR	SMART; SM00406;	IGv; 1.			
DR	PROSITE; PS50835;	IG LIKE; 1.			
KW	Immunoglobulin V region; Signal.				
FT	SIGNAL	1	19		
FT	CHAIN	20	144	Ig heavy chain V region MOPC 141.	
FT	DOMAIN	20	130	Ig-like.	
FT	NON TER	144	144		
SQ	SEQUENCE	144	AA; 15759	MW; 8E47A7CB3706D30A	CRC64;
Query Match					
Best Local Similarity		76.7%;	Score 487;	DB 1;	Length 144;
Matches 97;		Conservative 7;	Mismatches 14;	Indels 10;	Gaps 2;
QY	1	QVQLQESGPGLVAPSSLSITCTVSGISLNRYGVHWVRQPPGKGLVGLVITGGSTNYN	60		
		:	:	:	:
Db	20	QVQLKESGPGLVAPSSLSITCTVSGFSLTGYGVNWVRQPPGKGLVGLTIWNGSTDYN	79		
		:	:	:	:
QY	61	SALMSRLSISKDNKSQVFLKMNLSQTDDTAMYYCARDRSTMITAY-----AMDYWGQ	113		
		:	:	:	:
Db	80	STLKSRLTITKDNKSQVFLKMNLSQTDDTARYYCA---SVSIYYGRSDKYFTLDYWGQ	136		
		:	:	:	:
QY	114	GTTVTVSS	121		
		:	:		
Db	137	GTSVTVSS	144		
RESULT 4					
HV44_MOUSE					
ID	HV44_MOUSE	STANDARD;	PRT;	115	AA.
AC	P01820;				
DT	21-JUL-1986	(Rel. 01, Created)			
DT	21-JUL-1986	(Rel. 01, Last sequence update)			
DT	01-OCT-2004	(Rel. 45, Last annotation update)			
DE	Ig heavy chain V region PU14 precursor.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=81012133; PubMed=6774258;				

CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J03632; AAA49791.1; -.
DR PIR; B31933; B31933.
DR HSSP; P01820; 1A7N.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON TER 1
FT SIGNAL <1 18 Ig heavy chain V region XIG14.
FT CHAIN 19 135 Ig-like.
FT DOMAIN 20 128
FT NON TER 135 135
SQ SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;

Query Match 63.2%; Score 401.5; DB 1; Length 135;
Best Local Similarity 61.9%; Pred. No. 4.9e-34;
Matches 73; Conservative 19; Mismatches 23; Indels 3; Gaps 1;

QY 4 LQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWTGGSTNYSAL 63
Db 21 LQESGPGTVKPSFSLRLTCTVSGFELSSYHMHVIRQPPGKLEWIGVIATGGSTAIADSL 80

QY 64 MSRLSISKDNSKQVFLKMNLSLQTDITAMYYCARDRSTMITAYAMDYWGQTTVTSS 121
Db 81 KNRVTITKNGKKQVYLQMGMEVKDTAMYYCAREYA---SGYNFDYWGQGTMTVTTS 135

RESULT 7
Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 61.3%; Score 389.5; DB 2; Length 465;
Best Local Similarity 62.8%; Pred. No. 3.8e-32;
Matches 76; Conservative 17; Mismatches 23; Indels 5; Gaps 1;

QY 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWTGGSTNYN 60
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGISGYVWSWIRQPPAGKGLEWIGRIYTSNSTYN 79

QY 61 SALMSRLSISKDNSKQVFLKMNLSLQTDITAMYYCARDRSTMITAYAMDYWGQTTVTVS 120
Db 80 PSLKSRVTMSVDTSKNQFSLKLSVTAADTAIVYICARGRTY-----FDYWGQGTIVTVS 134

QY 121 S 121
Db 135 S 135

RESULT 8
BAD00255 PRELIMINARY; PRT; 129 AA.
ID BAD00255
AC BAD00255;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHDJ region (Fragment).
GN IGVH.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB091893; BAD00255.1; -.
FT NON TER 1
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14117 MW; D9642F5A5BE3BEEE CRC64;

Query Match 60.2%; Score 382; DB 2; Length 129;
Best Local Similarity 58.1%; Pred. No. 5.2e-32;
Matches 75; Conservative 20; Mismatches 26; Indels 8; Gaps 2;

QY 1 QVQLQESGPGLVAPQSLSITCTVSG--ISLNRYGVHVRQPPGKGLEWLGVIWTGGSTN 58
Db 1 QVQLQESGPGLVKPSQTLTLTCTVSGSITTSYYGWSWIRQPPGKGLEWMAIAYSGSTY 60

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073765; AAH73765.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;

Query Match 57.4%; Score 364.5; DB 2; Length 477;
Best Local Similarity 59.5%; Pred. No. 1.6e-29;
Matches 72; Conservative 17; Mismatches 29; Indels 3; Gaps 1;

QY 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVHWRQPPGKGLWLGVIWGGSTNYN 60
|||||
Db 20 QVQLQESGPGLVKPSLTSLTCTVSGGSISSYYWSWIRQACKGLEWIGYISHSGSTYN 79
|||||
QY 61 SALMSRLSISKDNKSQVFLKMNLSQTDDTAMYYCARDRSTMITAYAMDYWGQGTITVVS 120
:|||||
Db 80 PSLSKSRVTLSLDTSKNQFSLRLNSVTAAADTAVYYCAHGS---WDFAFDYWGQGITLVTS 136
|||||
QY 121 S 121
Db 137 S 137

RESULT 14
Q6P4I8
ID Q6P4I8 PRELIMINARY; PRT; 576 AA.
AC Q6P4I8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHD protein.
GN Name=IGHD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;

Query Match 57.4%; Score 364.5; DB 2; Length 576;
Best Local Similarity 62.3%; Pred. No. 2.1e-29;
Matches 76; Conservative 14; Mismatches 29; Indels 3; Gaps 2;

QY 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYG-VHWRQPPGKGLWLGVIWGGSTNY 59
|||||
Db 27 QVQLQESGPGLVKPSGTLTCAVSGGSISSNWSWVRQPPGKGLWIGEIYHSGSTNY 86
|||||
QY 60 NSALMSRLSISKDNKSQVFLKMNLSQTDDTAMYYCARDRSTMITAYAMDYWGQGTITVTV 119
:|||||
Db 87 NPSLSKSRVTISVDKSKNQFSLKLSVTAAADTAVYYCASLGD--IYYGMDVWGQGTITVTV 144
|||||
QY 120 SS 121
Db 145 SS 146

RESULT 15
AAH63384
ID AAH63384 PRELIMINARY; PRT; 576 AA.
AC AAH63384;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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OM protein - protein search, using sw model

Run on: October 13, 2004, 12:44:23 ; Search time 112.933 Seconds
(without alignments)
384.353 Million cell updates/sec

Title: US-10-049-868A-4
Perfect score: 635
Sequence: 1 QVQLQESGPGLVAPSQSLSI.....MITAYAMDYWGQTTVTVSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	87.7	113	2	AAR21268 Murine VH
2	555	87.4	115	8	ADF77174 Anti-VAP-
3	553	87.1	125	6	ABR44627 Murine va
4	547	86.1	667	6	ABP97414 Anti-huma
5	546	86.0	253	5	Aau72867 P5-9 sing
6	541.5	85.3	120	4	AAG63986 Amino aci
7	538	84.7	222	2	AAR32843 VH NQ2/12
8	538	84.7	235	2	AAR32840 VH NQ2/12
9	537	84.6	142	4	AAG66520 Mouse ant
10	535	84.3	119	2	AAY49218 Heavy cha
11	535	84.3	119	6	ADA14778 Peptide f
12	535	84.3	119	7	ADC35320 Anti-idio
13	534	84.1	123	2	AAW07438 Anti-DNA
14	534	84.1	269	2	AAR32569 Fusion pr
15	532	83.8	476	4	AAB49243 Chimeric
16	531.5	83.7	140	2	AAW22538 Murine an
17	531.5	83.7	140	5	AAE20201 Murine 44
18	531.5	83.7	140	8	ADJ31875 Murine 44
19	526	82.8	119	5	AAU72838 Anti-NKG2
20	525.5	82.8	242	2	AAR06483 18-2-3/TR
21	525.5	82.8	242	2	AAR43680 Single ch
22	525.5	82.8	242	2	AAR99650 Single ch
23	525.5	82.8	242	2	AAW02192 18-2-3/TR
24	523	82.4	119	2	AAW42451 Mouse ant
25	522.5	82.3	247	8	ADG28588 Paramyxov

26	522.5	82.3	287	6	ABR42057 Costimula
27	522.5	82.3	543	7	ADD12876 CD28/mela
28	521.5	82.1	112	2	AAW31648 Monoclonal
29	521.5	82.1	239	2	AAW02191 18-2-3/TR
30	521.5	82.1	241	2	AAR06482 18-2-3-/T
31	521	82.0	121	7	ADD25691 Binding d
32	521	82.0	271	7	ADD25693 Binding d
33	521	82.0	556	7	ADD25707 Binding d
34	520.5	82.0	239	2	AAR43679 Single ch
35	520.5	82.0	239	2	AAR99649 Single ch
36	519	81.7	119	6	ABJ19263 Anti-huma
37	519	81.7	279	6	ABJ19275 Anti-huma
38	518.5	81.7	116	2	AAR40951 Mouse ger
39	518	81.6	119	2	AAR98478 MAB 2B6 h
40	517.5	81.5	116	4	AAU07513 Antibody
41	517.5	81.5	239	2	AAW09813 Vlllys-lin
42	517.5	81.5	239	2	AAW35561 Ecor1-Hin
43	517.5	81.5	241	2	AAR21261 VHD1.3-Hu
44	517.5	81.5	267	2	AAR04841 Two linke
45	517.5	81.5	272	2	AAR21260 ScFV sequ

ALIGNMENTS

RESULT 1
AAR21268
ID AAR21268 standard; protein; 113 AA.
XX
AC AAR21268;
XX
DT 21-MAY-1992 (first entry)
XX
DE Murine VH group 2 chain E specific for phOx.
XX
KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
KW g3p; binding; adsorption; gene VIII; diverse repertoire;
KW specific binding pairs; replicable genetic display package.
XX
OS Synthetic.

Key Location/Qualifiers
FT Binding-site 31..35
FT /label= CDR1
FT Binding-site 50..65
FT /label= CDR2
FT Binding-site 98..102
FT /label= CDR3
FT /note= " D/N-X-G-X-X motif "
FT
FT
XX WO9201047-A.
XX
XX 23-JAN-1992.
XX
XX 10-JUL-1990; 90GB-00015198.
XX
XX 10-JUL-1990; 90GB-00015198.
XX 19-OCT-1990; 90GB-00022845.
XX 12-NOV-1990; 90GB-00024503.
XX 06-MAR-1991; 91GB-00004744.
XX 15-MAY-1991; 91GB-00010549.
XX
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX (MEDI-) MED RES COUNCIL.

XX
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD;
XX
XX WPI; 1992-056862/07.
XX
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic display
PT package.

XX Example 21; Fig 24; 209pp; English.

PS The VH sequence is one of eight (AAR21264-71) found to be expressed from

XX a single chain Fv library from an immunised mouse. The library produces a

CC diverse repertoire of antibody fragments specific for 2-phenyl-5-

CC oxazolone (phOx). It was prepd. using cDNA generated from mRNA from mice

CC immunised with phOx coupled to chicked serum albumin. The VH and VL kappa

CC sequences were separately amplified by PCR (see AAQ23474-84) and ligated

CC into fdCAT2 (see AAQ23463) for expression on the phage surface as fusions

CC with gene III. The resulting library of clones was diverse. Twenty three

CC hapten binding clones were sequenced revealing the eight different VH

CC genes (A-H) in a variety of pairings with seven different Vk genes (a-g)

CC (see AAR21264-92). Nearly all the VH genes belonged to gp 1, with only

CC one, "E", being of type "E". Most of the clones were Vk-d combinations. The

CC only one was of type "E". Of the twenty three clones sequenced, the

CC Kd of VH-B/Vk-d for phOx-GABA was 10 nM. Only two other combinations (of

CC eleven tested) were found to have higher values. This suggests that phage

CC bearing scFv fragments having weak affinities can be selected with

CC antigen, probably due to the avidity of the multiple antibody heads on

CC the phage. See also AAR21260-307, 309-311; AAR22450, 565-581

XX

SQ Sequence 113 AA;

Query Match 87.7%; Score 557; DB 2; Length 113;

Best Local Similarity 89.3%; Pred. No. 4.8e-44;

Matches 108; Conservative 0; Mismatches 5; Indels 8; Gaps 1;

QY 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLEWLVITGGSTNYN 60

Db 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLEWLVITGGSTNYN 60

QY 61 SALMSRLSISKDNSKQVFLKMNLSLQTDITAMYYCARDRSTMITAYAMDYWGQGTITVTS 120

Db 61 SALMSRLSISKDNSKQVFLKMNLSLQTDITAMYYCARDRG-----DYWGQGTITVTS 112

QY 121 S 121

Db 113 S 113

RESULT 2

ADF77174

ID ADF77174 standard; protein; 115 AA.

XX

AC ADF77174;

XX

DT 26-FEB-2004 (first entry)

XX

DE Anti-VAP-1 monoclonal antibody Mo1G6 H chain.

XX

DE complementarity determining region; CDR; mouse;

KW Vascular Adhesion Protein-1; VAP-1; antibody; heavy; light; chain;

KW chimeric; inflammatory disorder; rheumatoid arthritis;

KW inflammatory bowel disease; autoimmune disease; psoriasis;

KW immunosciintigraphic imaging.

XX

OS Mus sp.

XX

XX WO2003093319-A1.

XX

XX 13-NOV-2003.

PD

XX

XX 28-APR-2003; 2003WO-FI000330.

PF

XX

XX 29-APR-2002; 2002FI-00000807.

PR

XX

XX (BIOT-) BIOTIE THERAPIES CORP.

PA

XX

XX Jalkanen S, Salmi M, Laukkanen M, Clark MR;

PI

XX

XX WPI; 2004-022642/02.

DR

XX

PT New chimeric anti-Vascular Adhesion Protein-1 monoclonal antibodies and

PT encoding nucleic acid molecules, useful for diagnosing and treating

PT chronic inflammatory disorders, e.g. rheumatoid arthritis or psoriasis.

XX

PS Disclosure; Fig 1; 56pp; English.

XX

CC This sequence represents a heavy chain variable region from a mouse anti-

CC Vascular Adhesion Protein-1 (VAP-1) antibody. This sequence is included

CC in the specification for comparison with the antibody of the invention.

CC The murine antibody sequences of the invention may be used in the

CC production of a chimeric mouse-human anti-VAP-1 antibody. The nucleic

CC acid molecules, polypeptides or antibodies are useful in treating VAP-1

CC mediated inflammatory disorders, such as rheumatoid arthritis,

CC inflammatory bowel disease, autoimmune diseases or psoriasis. The

CC chimeric VAP-1 antibody is further used for in vitro and in vivo

CC diagnostic applications, including in vivo immunosciintigraphic imaging of

CC inflammation sites. The chimeric MAb's of the invention have improved

CC kinetic properties compared to the corresponding murine antibodies.

XX

SQ Sequence 115 AA;

Query Match 87.4%; Score 555; DB 8; Length 115;

Best Local Similarity 87.6%; Pred. No. 7.5e-44;

Matches 106; Conservative 4; Mismatches 5; Indels 6; Gaps 1;

QY 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLEWLVITGGSTNYN 60

Db 1 QVQLKESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLEWLVITGGSTNYN 60

QY 61 SALMSRLSISKDNSKQVFLKMNLSLQTDITAMYYCARDRSTMITAYAMDYWGQGTITVTS 120

Db 61 SALMSRLSISKDNSKQVFLKMNLSLQTDITAMYYCARD-----SYSFDYWGQGTITVTS 114

QY 121 S 121

Db 115 S 115

RESULT 3

ABR44627

ID ABR44627 standard; protein; 125 AA.

XX

AC ABR44627;

XX

DT 25-JUL-2003 (first entry)

XX

DE Murine variable heavy chain amino acid sequence MuVH1B.

XX

XX Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytostatic;

KW prostate specific membrane antigen; antipsoriatic; antiarthritic;

KW dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;

KW epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;

KW neoplastic disorder.

XX

OS Mus musculus.

OS Synthetic.

XX

XX WO2003024388-A2.

XX

XX 27-MAR-2003.

PD

XX

XX 30-MAY-2002; 2002WO-US017204.

PF

XX

XX 20-SEP-2001; 2001US-0324100P.

PR

XX

XX 08-MAR-2002; 2002US-0362612P.

PR

XX

XX (CORR) CORNELL RES FOUND INC.

PA

XX

XX Bander N;

PI

XX

XX WPI; 2003-313319/30.

DR

XX

XX Ablating/killing aberrant prostate specific membrane antigen-expressing

PT

PT cells for treating skin disorders, by contacting the cell with an
PT antibody that binds to the extracellular domain of prostate specific
PT membrane antigen.
XX
PS Disclosure; Fig 12B; 225pp; English.
XX
CC The present invention describes a method (M1) for ablating or killing an
CC aberrant prostate specific membrane antigen (PSMA)-expressing cell (e.g.
CC an epidermal and a dermal cell). M1 comprises contacting the cell, or a
CC vascular endothelial cell proximate to the cell, with an antibody (or its
CC antigen-binding fragment), which binds specifically to the extracellular
CC domain of PSMA in an amount sufficient to ablate or kill the cell. The
CC antibodies have antipsoriatic, antiarthritic, dermatological, cytostatic,
CC antiinflammatory and antiallergic activities, and can be used in
CC vaccines. M1 is useful for treating a skin disorder in a subject, by
CC administering to the subject, an amount of an antibody which binds
CC specifically to the extracellular domain of PSMA (the subject is a
CC mammal, preferably human and is having, or at risk of, a skin disorder).
CC The skin disorder is a dermal or an epidermal disorder, and is selected
CC from psoriasis (preferably chronic stationary psoriasis, psoriasis
CC vulgaris, eruptive (gluttate) psoriasis, psoriatic erythroderma,
CC generalised pustular psoriasis (Von Zumbusch), annular pustular
CC psoriasis, and localised pustular psoriasis), psoriatic arthritis,
CC exfoliative dermatitis, pityriasis rubra pilaris, pityriasis rosacea,
CC parapsoriasis, pityriasis lichenoides, lichen planus, lichen nitidus,
CC ichthyosiform dermatosis, keratodermas, dermatosis, and prokeratosis,
CC preferably psoriasis. M1 is useful for treating a skin disorder such as
CC an inflammatory or neoplastic disorder of the epidermis or dermis,
CC preferably an epidermal precancerous or cancerous lesion. M1 is also
CC useful to treat or prevent disorders involving aberrant activity of PSMA-
CC expressing cell, e.g. kidney, liver or brain cell. ACC69816 to ACC69837
CC and ABR44613 to ABR44733 represent sequences used in the exemplification
CC of the present invention
XX
SQ Sequence 125 AA;

Query Match 87.1%; Score 553; DB 6; Length 125;
Best Local Similarity 87.2%; Pred. No. 1.3e-43;
Matches 109; Conservative 3; Mismatches 9; Indels 4; Gaps 2;

QY 1 QVQLQESGPGLVAPQSLSITCTVSGISLNRYGVH--WVRQPPGKGLEWLGVIWTCGSTN 58
Db :|||||
1 QVQLKESGPGLVAPQSLSITCTVSGFSLTSYGVHVSWVRQPPGKGLEWLGVIWAGGSTN 60
QY 59 YNSALMSRLSISKDNKSQVFLKWNLSQTDTDAMYVCARDRSTMITA--YAMDYWGQGT 116
Db :|||||
61 YNSALMSRLSISKDNKSQVFLKWNLSQTDTDAMYVCARDRGRYYYSGYAMDYWGQGTS 120

QY 117 VTVSS 121
Db :|||
121 VTVSS 125

RESULT 4
ABP97414
ID ABP97414 standard; protein; 667 AA.
XX
AC ABP97414;
XX

DT 30-MAY-2003 (first entry)

DE Anti-human seminal plasma protein ScFv/hCPA fusion protein.

XX
KW Single chain antibody; ScFv; anti-human seminal plasma protein;
KW monoclonal antibody E4B7; mouse; murine; human; carboxypeptidase A; hCPA;
KW fusion protein; antibody-directed enzyme prodrug therapy; ADEPT;
KW methotrexate-alpha-peptide prodrug; prostate cancer; cytostatic; gene;
KW ds.
XX

OS Mus musculus.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.

XX
FH Location/Qualifiers
FT 1. .245
FT /label= E4B7 derived ScFv
FT /note= "Anti-human seminal plasma protein single chain
FT antibody derived from murine monoclonal antibody E4B7 VH
FT and VL regions; targets fusion protein to prostate cancer
FT cells"
FT 1. .122
FT /note= "Corresponds to monoclonal antibody E4B7 VH (heavy
FT chain variable region"
FT 123. .137
FT /label= ScFv_linker
FT 138. .245
FT /note= "Corresponds to monoclonal antibody E4B7 VL (light
FT chain variable region"
FT Misc-difference 216
FT /note= "Encoded by GAC"
FT 245. .251
FT /label= ScFv/hCPA_linker
FT Misc-difference 247
FT /note= "Encoded by AGC"
FT 253. .667
FT /label= hCPA
FT /note= "Human carboxypeptidase A; activates methotrexate-
FT alpha-peptide prodrug"

WO2002100431-A1.

19-DEC-2002.

08-JUN-2001; 2001WO-CN000924.

08-JUN-2001; 2001WO-CN000924.

(UYTA-) UNIV TANGDU HOSPITAL FORTH MILITARY MEDI.
(HAOX/) HAO X.

Hao X;

WPI; 2003-156924/15.
N-PSDB; ABZ75116.

Pharmaceutical kits for use in the treatment of prostate cancer, comprise
anti-human seminal plasma protein single-chain antibody/human
carboxypeptidase fusion protein and a prodrug of methotrexate-alpha-
peptides.

Claim 3; Fig 4; 29pp; Chinese.

The invention relates to a pharmaceutical kit for antibody-directed
enzyme prodrug therapy (ADEPT) to treat prostate cancer. The kit
comprises several respective containers for holding anti-human seminal
plasma protein single-chain antibody (ScFv)/human carboxypeptidase A
(hCPA) fusion protein (ABP97414), a prodrug of methotrexate-alpha-peptide
and a pharmaceutically-acceptable auxiliary for medication. The invention
also encompasses the anti-human seminal plasma protein ScFv/hCPA fusion
protein, and the nucleic acid encoding it (ABZ75116). This was
constructed by linking DNA encoding the ScFv (itself generated by linking
DNAs encoding the heavy and light chain variable regions (VH and VL) of
the murine anti-human seminal plasma protein monoclonal antibody E4B7) to
DNA encoding human carboxypeptidase A via a linker. The ScFv portion of
the fusion protein enables it to be specifically targeted to prostate
cancer cells, where the hCPA portion can then activate the prodrug which
in turn has cytostatic activity towards the cancer cells. The invention
permits the fusion protein to be easily produced in large quantities for
use in ADEPT for prostate cancer treatment. The present sequence
represents the ScFv/hCPA fusion protein of the invention

Sequence 667 AA;

Query Match 86.1%; Score 547; DB 6; Length 667;
Best Local Similarity 86.8%; Pred. No. 3e-42;

XX The sequences given in AAR32840-43 show the mature heavy chain VH domains
CC and the Vk light chain genes of the antiphenyloxazalone hybridomas
CC NQ2/12.4 and NQ10/12.5 which have been linked via a linker peptide by in-
CC cell PCR. The cDNA encoding these peptides was synthesised using forward
CC primers annealing to the Ck gene and the JH segment, followed by assembly
CC with linker primers, VH back primers based on the VH3 leader sequence and
CC a forward Ck primer nested in respect to the primer used for cDNA. The
CC assembled product within the cells is then amplified with nested primers
CC annealing to the 5' end of the VH gene and the 3' end of the Jk segment.
CC In-cell PCR may be used to determine gene linkage analysis, particularly
CC for the cloning of gene combinations that are polymorphic within a
CC population of cells, such as the rearranged genes for Ig or TCR V
CC regions. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 235 AA;

Query Match 84.7%; Score 538; DB 2; Length 235;
Best Local Similarity 86.0%; Pred. No. 6.3e-42;
Matches 104; Conservative 2; Mismatches 7; Indels 8; Gaps 1;

QY 1 QVQLQESGPGGLVAPSQSLISITCTVSGISLNRYGVHWVRQPPGKGLEWLGVIWTGGSTNYN 60
Db 1 QVQLKESGPGGLVAPSQSLISITCTVSGFSLTSYGVHWVRQPPGKGLEWLGVIWAGGSTNYN 60
QY 61 SALMSRLSISKDNSKSVFLKMNLSLOTDDTAMYYCARDRSTMITAYAMDYWGQGTTVTVS 120
Db 61 SALMSRLSISKDNSKSVFLKMNLSLOTDDTAMYYCARDRGA-----YWGQGTLLTVTS 112
QY 121 S 121
Db 113 A 113

RESULT 9
AAG66520
ID AAG66520 standard; protein; 142 AA.
XX
AC AAG66520;
XX
DT 22-OCT-2001 (first entry)
XX
DE Mouse antibody 26 heavy chain variable region.
XX
KW Mouse; CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4;
KW immunosuppressive; immunomodulator; antiallergic; vaccine; antibody;
KW T cell; humanised antibody; autoimmune disorder; graft rejection;
KW allergy; antibody 26; heavy chain variable region; VH.
XX
OS Mus musculus.
XX
PN WO200154732-A1.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US002653.
XX
PR 27-JAN-2000; 2000US-0178473P.
XX
PA (GEMY) GENETICS INST INC.
XX
XX Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;
PI O'hara D, Hinton P, Tsurushita N;
XX
XX WPI; 2001-483195/52.
DR N-PSDB; AAH76438.
XX
XX Novel antibody-toxic group conjugate comprising an antibody that
PT recognizes a molecule expressed only on activated T cells, useful for
PT modulating immune response for treating autoimmune disorder, allergic
PT response.
XX
PS Example 7; Page 84; 123pp; English.

XX The invention relates to an antibody-toxic group conjugate comprising an
CC antibody that specifically recognises a molecule expressed only on
CC activated T cells, and a toxic group. The T cell molecule is preferably
CC human cytotoxic T lymphocyte associated antigen 4 (CTLA4). The antibody
CC of the invention is a humanised anti-CTLA4 antibody comprising a sequence
CC of 128 or 142 amino acids fully defined in the specification. The
CC antibody-toxic group conjugate is useful for modulating the immune
CC response in a subject suffering from a disorder or condition such as
CC autoimmune disorder, immune response to a graft, allergic response or an
CC immune response to a therapeutic protein. The antibody is also useful for
CC research purposes, e.g., in staining and isolating CTLA4-bearing cells.
CC The antibody is also useful for T-cell typing, for isolating specific IL-
CC 2 receptor-bearing cells or fragments of the receptor, for vaccine
CC preparation, and for determining the effectiveness of an agent to down-
CC regulate CTLA4 activity. The present sequence is the heavy chain variable
CC region of mouse antibody 26. It was used in the construction of the
CC humanised anti-CTLA4 antibody of the invention
XX
SQ Sequence 142 AA;

Query Match 84.6%; Score 537; DB 4; Length 142;
Best Local Similarity 84.6%; Pred. No. 4.5e-42;
Matches 104; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

QY 1 QVQLQESGPGGLVAPSQSLISITCTVSGISLNRYGVHWVRQPPGKGLEWLGVIWTGGSTNYN 60
Db 20 QVQLKESGPGGLVAPSQSLISITCTVSGFSLTSYGVHWVRQPPGKGLEWLGVIWAGGSTNYN 79
QY 61 SALMSRLSISKDNSKSVFLKMNLSLOTDDTAMYYCAR--DRSTMITAYAMDYWGQGTTVT 118
Db 80 SALMSRLSISKDNSKSVFLKMNLSLOTDDTAMYYCARGPPHAMMKRGYAMDYWGQGTSVI 139
QY 119 VSS 121
Db 140 VSS 142

RESULT 10
AAY49218
ID AAY49218 standard; protein; 119 AA.
XX
AC AAY49218;
XX
DT 07-FEB-2000 (first entry)
XX
DE Heavy chain variable region consensus sequence.
XX
KW Monoclonal antibody; Mab; 1A7; GD2; immune response; melanoma;
KW neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma;
KW tumor-associated antigen.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 99..102 /note= "residues Xaa are unspecified"
FT
XX US5977316-A.
XX
XX 02-NOV-1999.
XX
XX 16-JAN-1996; 96US-00591196.
XX
XX 17-JAN-1995; 95US-00372676.
XX (KENT) UNIV KENTUCKY.
XX
XX Foon KA, Chatterjee SK, Chatterjee M;
XX WPI; 1996-354530/35.
XX
XX Monoclonal antibody 1A7 and related polynucleotide(s) and polypeptide(s)
PT

PT - useful to treat or palliate a GD2-associated disease, e.g. melanoma and glioma.

XX Disclosure; Fig 3C; 74pp; English.

CC The invention provides a monoclonal antibody (MAB) designated 1A7, which elicits an anti-GD2 (tumor-associated antigen) immunological response in humans. MAB 1A7 has defined light and heavy chain variable region sequences. The MAB 1A7 and polypeptides can be used for eliciting an anti -GD2 immune response. The polypeptides can also be used for detecting or purifying anti-GD2 antibody. The products can be used for treating GD2 - associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue carcinoma, and small cell carcinoma. They can be used for palliating the disease or for reducing the risk of recurrence. The present sequence CC represents the heavy chain variable region consensus sequence

XX Sequence 119 AA;

Query Match 84.3%; Score 535; DB 2; Length 119;
Best Local Similarity 86.0%; Pred. No. 5.6e-42;
Matches 104; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVAPSQSLSICTVSGISLNRYGVHVRQPPGKLEWLGVIWGGSTNYN 60
Db 1 QVQLKESGPGLVAPSQSLSICTVSGFSLTSYGVHVRQPPGKLEWLGVIWGGSTNYN 60
QY 61 SALMSRLSISKDNSKQVFLKMNSLQDDTAMYYCARDSTMITAYAMDYWGQGTITVVS 120
Db 61 SALKSRLSISKDNSKQVFLKMNSLQDDTARYYCAREXXX--XYYAMDYWGQGTITVVS 118
QY 121 S 121
Db 119 S 119

RESULT 11
ADA14778
ID ADA14778 standard; peptide; 119 AA.

XX ADA14778;
XX 06-NOV-2003 (first entry)
XX Peptide from antibody heavy chain resembling 1A7 #7.
KW heavy chain variable region; mouse; ganglioside GD2-associated tumour;
KW melanoma; antibody; anti-idiotypic; monoclonal antibody; 1A7;
KW neuroblastoma; glioma; sarcoma; small cell lung cancer.

OS Mus sp.
XX US6509016-B1.
XX 21-JAN-2003.
XX 15-APR-1999; 99US-00293533.
PR 17-JAN-1995; 95US-00372676.
PR 16-JAN-1996; 96US-00591196.
PR 21-NOV-1996; 96US-00752844.

XX (KENT) UNIV KENTUCKY.
XX Chatterjee M, Foon KA, Chatterjee SK;
XX WPI; 2003-401117/38.

XX Delaying recurrence and/or development of ganglioside GD2-associated tumor in individual, by administering antibody containing light and heavy chain variable region sequences contained in sequence of specified amino acids.

PS Example 2; Fig 3; 82pp; English.

XX The invention relates to the recurrence and/or development of a ganglioside GD2-associated tumour, e.g. melanoma, in an individual which is delayed by administration of an antibody comprising light and heavy chain variable region sequences of the anti-idiotypic monoclonal antibody 1A7. The antibody is used for delaying recurrence and/or development of GD2-associated tumour, e.g. melanoma, neuroblastoma, glioma, sarcoma, or small cell lung cancer, in individual, and for treating individual with GD2-associated tumour. The present sequence is a unique peptide region from an antibody sequence resembling the anti-idiotypic antibody 1A7 heavy chain.

XX Sequence 119 AA;

Query Match 84.3%; Score 535; DB 6; Length 119;
Best Local Similarity 86.0%; Pred. No. 5.6e-42;
Matches 104; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVAPSQSLSICTVSGISLNRYGVHVRQPPGKLEWLGVIWGGSTNYN 60
Db 1 QVQLKESGPGLVAPSQSLSICTVSGFSLTSYGVHVRQPPGKLEWLGVIWGGSTNYN 60
QY 61 SALMSRLSISKDNSKQVFLKMNSLQDDTAMYYCARDSTMITAYAMDYWGQGTITVVS 120
Db 61 SALKSRLSISKDNSKQVFLKMNSLQDDTARYYCAREXXX--XYYAMDYWGQGTITVVS 118
QY 121 S 121
Db 119 S 119

RESULT 12
ADC35320
ID ADC35320 standard; protein; 119 AA.

XX ADC35320;
XX 18-DEC-2003 (first entry)
XX Anti-idiotypic antibody VH region consensus sequence.
KW Mouse; monoclonal antibody; 1A7; anti-idiotypic antibody; ganglioside GD2;
KW cytostatic; melanoma; neuroblastoma; small cell lung cancer; tumour;
KW antibody; variable region; VH; VL; glioma; soft tissue sarcoma; vaccine.

OS Synthetic.
OS Mus sp.
XX US2003114398-A1.
XX 19-JUN-2003.
XX 21-MAY-2002; 2002US-00153401.
XX 17-JAN-1995; 95US-00372676.
PR 16-JAN-1996; 96US-00591196.
PR 15-APR-1999; 99US-00293533.

XX (CHAT/) CHATTERJEE M.
XX (FOON/) FOON K A.
XX (CHAT/) CHATTERJEE S K.

XX Chatterjee M, Foon KA, Chatterjee SK;
XX WPI; 2003-810913/76.

XX Novel anti-idiotypic monoclonal antibody 1A7, that is capable of recruiting a tumor-specific response against glycosphingolipid GD2, useful for treating a GD2-associated disease e.g., melanoma, glioma, soft tissue sarcoma.

XX Example 2; SEQ ID NO 16; 84pp; English.

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 12:59:19 ; Search time 87.2208 Seconds
(without alignments)
447.653 Million cell updates/sec

Title: US-10-049-868A-4
Perfect score: 635
Sequence: 1 QVQLQESGPGLVAPSQSLSI.....MITAYAMDYWGQTTVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1356558 seqs, 322682953 residues

Total number of hits satisfying chosen parameters: 1356558

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	87.7	113	16	US-10-803-622-218
2	557	87.7	113	16	US-10-803-622-218
3	546	86.0	253	15	US-10-239-656-63
4	537	84.6	142	9	US-09-772-103-4
5	535	84.3	119	14	US-10-153-401-16
6	532	83.8	476	16	US-10-660-128-12
7	531.5	83.7	140	8	US-08-973-518-4
8	531.5	83.7	140	9	US-09-007-093-4
9	531.5	83.7	140	14	US-10-428-754-4
10	531	83.6	119	14	US-10-232-187-2
11	526	82.8	119	15	US-10-239-656-23
12	523	82.4	119	14	US-10-144-644-15
13	523	82.4	119	16	US-10-700-740-15
14	521.5	82.1	112	9	US-09-824-286-3
					Sequence 218, App
					Sequence 218, App
					Sequence 63, Appl
					Sequence 4, Appli
					Sequence 16, Appl
					Sequence 12, Appl
					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 2, Appli
					Sequence 23, Appl
					Sequence 15, Appl
					Sequence 15, Appl
					Sequence 3, Appli

15	521	82.0	121	14	US-10-207-655-252	Sequence 252, App
16	521	82.0	271	14	US-10-207-655-254	Sequence 254, App
17	521	82.0	556	14	US-10-207-655-268	Sequence 268, App
18	517.5	81.5	116	14	US-10-169-351-108	Sequence 108, App
19	517.5	81.5	241	16	US-10-803-622-187	Sequence 187, App
20	517.5	81.5	241	16	US-10-803-653-187	Sequence 187, App
21	517.5	81.5	272	16	US-10-803-622-183	Sequence 183, App
22	517.5	81.5	272	16	US-10-803-653-183	Sequence 183, App
23	515.5	81.2	120	14	US-10-194-975-112	Sequence 112, App
24	514.5	81.0	116	14	US-10-194-975-100	Sequence 100, App
25	510.5	80.4	135	16	US-10-351-748-31	Sequence 31, Appl
26	510.5	80.4	135	17	US-10-351-748-31	Sequence 31, Appl
27	508.5	80.1	333	14	US-10-059-261-61	Sequence 61, Appl
28	505.5	79.6	139	8	US-08-779-784-37	Sequence 37, Appl
29	505.5	79.6	241	15	US-10-353-721-13	Sequence 13, Appl
30	503	79.2	249	9	US-09-730-374-3	Sequence 3, Appli
31	503	79.2	249	16	US-10-704-206-3	Sequence 3, Appli
32	502	79.1	121	11	US-09-842-776A-52	Sequence 52, Appl
33	501.5	79.0	116	15	US-10-435-299-4	Sequence 4, Appli
34	501.5	79.0	118	14	US-10-056-052-16	Sequence 16, Appl
35	500	78.7	121	14	US-10-056-052-12	Sequence 12, Appl
36	494.5	77.9	119	13	US-10-140-555-2	Sequence 2, Appli
37	494.5	77.9	139	9	US-09-881-823-4	Sequence 4, Appli
38	493.5	77.7	120	16	US-10-697-399-5	Sequence 5, Appli
39	491.5	77.4	135	14	US-10-010-729-68	Sequence 68, Appl
40	490.5	77.2	116	16	US-10-682-845-53	Sequence 53, Appl
41	490.5	77.2	492	16	US-10-682-845-59	Sequence 59, Appl
42	490.5	77.2	492	16	US-10-682-845-61	Sequence 61, Appl
43	490.5	77.2	492	16	US-10-682-845-63	Sequence 63, Appl
44	490.5	77.2	492	16	US-10-682-845-65	Sequence 65, Appl
45	490.5	77.2	492	16	US-10-682-845-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-10-803-622-218
; Sequence 218, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,622
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134

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; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 218
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-218

Query Match      87.7%; Score 557; DB 16; Length 113;
Best Local Similarity 89.3%; Pred. No. 2e-46;
Matches 108; Conservative 0; Mismatches 5; Indels 8; Gaps 1;

QY      1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWTGGSTNYN 60
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QY      61 SALMSRLSISKDNSKSVFLKMNSLQTDTTAMYYCARDRSTMITAYAMDYWGQTTVTVS 120
Db      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 SALMSRLSISKDNSKSVFLKMNSLQTDTTAMYYCARDRG-----DYWGQTTVTVS 112

QY      121 S 121
Db      113 S 113

RESULT 2
US-10-803-653-218
; Sequence 218, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,653
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
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; PRIOR FILING DATE: 1995-06-07
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; SEQ ID NO 218
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-218

Query Match      87.7%; Score 557; DB 16; Length 113;
Best Local Similarity 89.3%; Pred. No. 2e-46;
Matches 108; Conservative 0; Mismatches 5; Indels 8; Gaps 1;

QY      1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWTGGSTNYN 60
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QY      61 SALMSRLSISKDNSKSVFLKMNSLQTDTTAMYYCARDRSTMITAYAMDYWGQTTVTVS 120
Db      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 SALMSRLSISKDNSKSVFLKMNSLQTDTTAMYYCARDRG-----DYWGQTTVTVS 112

QY      121 S 121
Db      113 S 113

RESULT 3
US-10-239-656-63
; Sequence 63, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTTERBUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOFWEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; TITLE OF INVENTION: TO AN EPITOPE OF THE NKG2D RECEPTOR COMPLEX
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
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; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic P5-3 single
; OTHER INFORMATION: chain Fv
US-10-239-656-63

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Db 118 SS 119

RESULT 4

US-09-772-103-4

; Sequence 4, Application US/09772103

; Publication No. US20020039581A1

; GENERAL INFORMATION:

; APPLICANT: Carreno, Beatriz M.

; APPLICANT: Wood, Clive

; APPLICANT: Turner, Katherine

; APPLICANT: Collins, Mary

; APPLICANT: Gray, Gary S.

; APPLICANT: Morris, Donna

; APPLICANT: O'Hara, Denise

; APPLICANT: Hinton, Paul

; APPLICANT: Tsurushita, Naoya

; TITLE OF INVENTION: ANTIBODIES AGAINST CTLA4 AND USES THEREFOR

; FILE REFERENCE: GNN-009CP

; CURRENT APPLICATION NUMBER: US/09/772,103

; CURRENT FILING DATE: 2001-01-23

; PRIOR APPLICATION NUMBER: 60/178,473

; PRIOR FILING DATE: 2000-01-27

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 142

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-772-103-4

Query Match 84.6%; Score 537; DB 9; Length 142;

Best Local Similarity 84.6%; Pred. No. 2.3e-44;

Matches 104; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

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Db 80 SALMSRLSISKDNSKQVFLKMSLQTDTTAMYCCARGPPHAMMKRGYAMDYWGQGTSVI 139

QY 119 VSS 121

Db 140 VSS 142

RESULT 5

US-10-153-401-16

; Sequence 16, Application US/10153401

; Publication No. US20030114398A1

; GENERAL INFORMATION:

; APPLICANT: Chatterjee, Malaya

; Foon, Kenneth A.

; Chatterjee, Sunil K.

; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 PAGE MILL ROAD

; CITY: PALO ALTO

; STATE: CA

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/153,401

; FILING DATE: 27-Aug-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 09/293,533

; FILING DATE: 1999-04-15

; APPLICATION NUMBER: US 08/372,676

; FILING DATE: 1995-01-17

; APPLICATION NUMBER: US 08/591,196

; FILING DATE: 1996-01-16

; ATTORNEY/AGENT INFORMATION:

; NAME: Catherine M. Polizzi

; REGISTRATION NUMBER: 40,130

; REFERENCE/DOCKET NUMBER: 304142000202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 813-5600

; TELEFAX: (415) 494-0792

; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 119 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-10-153-401-16

Query Match 84.3%; Score 535; DB 14; Length 119;

Best Local Similarity 86.0%; Pred. No. 2.9e-44;

Matches 104; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVAPSQSLSTCTVSGISLNRYGVHVRQPPGKGLEWLGVIWGTGGSTNYN 60

Db 1 QVQLKESGPGLVAPSQSLSTCTVSGFSLTSYGVHVRQPPGKGLEWLGVIWGDGSTNYN 60

QY 61 SALMSRLSISKDNSKQVFLKMSLQTDTTAMYCARDSTRMTITAYAMDYWGQGTTVTS 120

Db 61 SALKSRLSISKDNSKQVFLKMSLQTDTTARYYCAREXXX--XYAMDYWGQGTSTVTS 118

QY 121 S 121

Db 119 S 119

RESULT 6

US-10-660-128-12

; Sequence 12, Application US/10660128

; Publication No. US20040120947A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Chuntharapai, Anan

; APPLICANT: Dodge, Kelly

; APPLICANT: Kim, Kyung Jin

; TITLE OF INVENTION: DR4 Antibodies and Uses Thereof

; FILE REFERENCE: P1245RIP2B

; CURRENT APPLICATION NUMBER: US/10/660,128

; CURRENT FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US/09/584,166

; PRIOR FILING DATE: 2000-05-25

; PRIOR APPLICATION NUMBER: US 09/322,875

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: US 09/237,299

; PRIOR FILING DATE: 1999-01-25

; PRIOR APPLICATION NUMBER: US 60/072,481

; PRIOR FILING DATE: 1998-01-26

; NUMBER OF SEQ ID NOS: 12

; SEQ ID NO 12

; LENGTH: 476

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Sequence is synthesized.


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RESULT 9
US-10-428-754-4
; Sequence 4, Application US/10428754
; Publication No. US20030228304A1
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; Barber, Brian H
; Cates, George A
; Caterini, Judith E
; Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/428,754
; FILING DATE: 05-May-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 10/428,754
; FILING DATE: 05-MAY-2003
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-1065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-428-754-4
Query Match 83.7%; Score 531.5; DB 14; Length 140;
Best Local Similarity 85.1%; Pred. No. 7.6e-44;
Matches 103; Conservative 4; Mismatches 13; Indels 1; Gaps 1;
QY 1 QVQLQESGPGLVAPSQSLSTCTVSGISLNRYGVHWRQPPGKGLEWLGVIWGGSTNYN 60
Db 21 QVQLKESGPGLVAPSQSLSTCTVSGFSLTSYGVHWRQPPGKGLEWLGVIWAGGSINYN 80
QY 61 SALMSRLSISKDNKSQVFLKMNLSLQDDTAMYYCARDRSTMITAYAMDYWGQGTITVTS 120
Db 81 SALMSRLSISKDNFKSQVFLKMNSSLQDDTAMYYCARAYGDYV-HYAMDYWGQGTISVTAS 139
QY 121 S 121
Db 140 S 140
RESULT 10
US-10-232-187-2
; Sequence 2, Application US/10232187
; Publication No. US20030092091A1
; GENERAL INFORMATION:
; APPLICANT: Abrahamson, Julie A.
```

```
; APPLICANT: Bochner, Bruce
; APPLICANT: Erickson-Miller, Connie L.
; APPLICANT: Kikly, Kristine K.
; APPLICANT: Schleimer, Robert
; APPLICANT: Nulku, Turkan E.
; TITLE OF INVENTION: Sialcadhesin Factor-2 Antibodies
; FILE REFERENCE: GH50042-1
; CURRENT APPLICATION NUMBER: US/10/232,187
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/187,595
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: PCT/US01/07193
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/315,943
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/349,830
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/394,741
; PRIOR FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-232-187-2
Query Match 83.6%; Score 531; DB 14; Length 119;
Best Local Similarity 86.0%; Pred. No. 7.1e-44;
Matches 104; Conservative 7; Mismatches 8; Indels 2; Gaps 2;
QY 1 QVQLQESGPGLVAPSQSLSTCTVSGISLNRYGVHWRQPPGKGLEWLGVIWGGSTNYN 60
Db 1 QVQLKESGPGLVAPSQSLSTCTVSGFSL-IYGAHWVRQPPGKGLEWLGVIWAGGSN 59
QY 61 SALMSRLSISKDNKSQVFLKMNLSLQDDTAMYYCARDRSTMITAYAMDYWGQGTITVTS 120
Db 60 SALMSRLSISKDNKSQVFLKINSLQDDTALYYCARDGSSPY-YYSMEYWGQGTISVTVS 118
QY 121 S 121
Db 119 S 119
RESULT 11
US-10-239-656-23
; Sequence 23, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTTERBUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOFMEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Anti-NKG2D
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OTHER INFORMATION: hybridoma 6H7E7 variable heavy chain
US-10-239-656-23

Query Match 82.8%; Score 526; DB 15; Length 119;
Best Local Similarity 86.0%; Pred. No. 2.2e-43;
Matches 104; Conservative 1; Mismatches 14; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWTGGSTNYN 60
Db 1 QVQLQESGPGLVAPSQSLITCTVSGFSLTSYGVHWIRQPPGKGLEWLGVIWAGGSTNYN 60
QY 61 SALMSRLSISKDNKSQVFLKMNLSLOTDDTAMYYCARDRSTMITAYAMDYWGQGTITVTVS 120
Db 61 SALMSRLSISKDNKSQVFLKMNLSLQIDDTAMYYCA--RGGYEGAAWFGYWGQGTITVTVS 118

QY 121 S 121
Db 119 S 119

RESULT 12
US-10-144-644-15
Sequence 15, Application US/10144644
Publication No. US20030059429A1
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders

NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp
STREET: P.O. Box 1539-UW2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/144,644
FILING DATE: 2002-08-08
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467420
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION: INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-144-644-15

Query Match 82.4%; Score 523; DB 14; Length 119;
Best Local Similarity 82.6%; Pred. No. 4.2e-43;
Matches 100; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWTGGSTNYN 60
Db 1 QVQLKESGPGLVAPSQSLITCTVSGFSLTSYSVHWVRQPPGKGLEWLGVIWASGGTDYN 60
QY 61 SALMSRLSISKDNKSQVFLKMNLSLOTDDTAMYYCARDRSTMITAYAMDYWGQGTITVTVS 120
Db 61 SALMSRLSISKDNKSQVFLKMNLSLOTDDTAMYYCARDPPSSL--LRLDYWGQGTITLTVS 118

QY 121 S 121
Db 119 S 119

RESULT 13
US-10-700-740-15
Sequence 15, Application US/10700740
Publication No. US20040156850A1
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders

NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp
STREET: P.O. Box 1539-UW2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/700,740
FILING DATE: 04-Nov-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/144,644
FILING DATE: 2002-08-08
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/467420
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-700-740-15

Query Match 82.4%; Score 523; DB 16; Length 119;
Best Local Similarity 82.6%; Pred. No. 4.2e-43;
Matches 100; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVVRRQPPGKGLEWLGVIWGGSTNYN 60
Db 1 QVQLKESGPGLVAPSQSLITCTVSGFSLTSYSVHVVRRQPPGKGLEWLGVIWASGGTDYN 60
QY 61 SALMSRLSISKDNKSQVFLKMNSLQTDGTTAMYYCARDRSTMITAYAMDYWGQTTVTVS 120
Db 61 SALMSRLSISKDNKSQVFLKLNSLQTDGTTAMYYCARDPPSSL--LRLDYWGQTTLTVS 118
QY 121 S 121
Db 119 S 119

RESULT 14
US-09-824-286-3
Sequence 3, Application US/09824286
Patent No. US20020028202A1
GENERAL INFORMATION:

APPLICANT: Burkly, Linda C
Benjamin, Christopher D
Hession, Catherine A
Whitty, Adrian
TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Biogen, Inc.
STREET: 14 Cambridge Center
City: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02142

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/824,286
FILING DATE: 02-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017,466
FILING DATE: 10-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kaplan, Warren A.
REGISTRATION NUMBER: 34,199
REFERENCE/DOCKET NUMBER: A006 PCT CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 679-2000
TELEFAX: 617 679-2838

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-824-286-3
Query Match 82.1%; Score 521.5; DB 9; Length 112;
Best Local Similarity 85.2%; Pred. No. 5.5e-43;

Matches 98; Conservative 8; Mismatches 6; Indels 3; Gaps 1;
QY 4 LOESGPGLVAPSQSLITCTVSGISLNRYGVHVVRRQPPGKGLEWLGVIWGGSTNYNSAL 63
Db 1 LOESGPGLVAPSQSLITCTVSGFSLTSYGVHVVRRQPPGKGLEWLGVIWAGGSTNYNSAL 60
QY 64 MSRLSISKDNKSQVFLKMNSLQTDGTTAMYYCARDRSTMITAYAMDYWGQTTVT 118
Db 61 MSRLNINRDNKSQIFLKMNSLQTDGTTAIYYCAREGSTV---DSMDYWGQTTVT 112

RESULT 15
US-10-207-655-252
Sequence 252, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 252
LENGTH: 121
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion polypeptide
US-10-207-655-252

Query Match 82.0%; Score 521; DB 14; Length 121;
Best Local Similarity 82.6%; Pred. No. 6.7e-43;
Matches 100; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHVVRRQPPGKGLEWLGVIWGGSTNYN 60
Db 1 QVQLKESGPGLVAPSQSLITCTVSGFSLTSYGVHVVRRQPPGKGLEWLGVIWGGSTNYN 60
QY 61 SALMSRLSISKDNKSQVFLKMNSLQTDGTTAMYYCARDRSTMITAYAMDYWGQTTVTVS 120
Db 61 SALKSRLSITKDNKSQVFLKMNSLQTDGTTARYYCARDGYSNFHYVMDYWGQTSVTVS 120
QY 121 S 121
Db 121 S 121

Search completed: October 13, 2004, 13:15:28
Job time : 88.2208 secs

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Db 1 QVQLKESGPGLVAPSQSLITCTVSGFSLTSYGVHWVRQPPGKGLEWLGVWAGGSTNYN 60
Qy 61 SALMSRLSISKDNKSQVFLKMNLSQTDDTAMYYCARDRSTMITAYAMDYWGQGTITVTS 120
Db 61 SALMSRLSISKDNKSQVFLKMNLSQTDDTAMYYCARDRGA-----YWGQGTITVTS 112
Qy 121 S 121
Db 113 A 113

RESULT 2
US-08-190-199A-61
; Sequence 61, Application US/08190199A
; Patent No. 5830663
; GENERAL INFORMATION:
; APPLICANT: EMBLETON, Michael J.
; APPLICANT: GOROCHOV, Guy
; APPLICANT: JONES, Peter T.
; APPLICANT: WINTER, Gregory P.
; TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,199A
; FILING DATE: 13-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/01483
; FILING DATE: 10-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9212419.7
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9117352.6
; FILING DATE: 10-AUG-1991
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-190-199A-61

Query Match 84.7%; Score 538; DB 2; Length 235;
Best Local Similarity 86.0%; Pred. No. 7.4e-48;
Matches 104; Conservative 2; Mismatches 7; Indels 8; Gaps 1;

Qy 1 QVQLKESGPGLVAPSQSLITCTVSGFSLTSYGVHWVRQPPGKGLEWLGVWAGGSTNYN 60
Db 1 QVQLKESGPGLVAPSQSLITCTVSGFSLTSYGVHWVRQPPGKGLEWLGVWAGGSTNYN 60
Qy 61 SALMSRLSISKDNKSQVFLKMNLSQTDDTAMYYCARDRSTMITAYAMDYWGQGTITVTS 120
Db 61 SALMSRLSISKDNKSQVFLKMNLSQTDDTAMYYCARDRGA-----YWGQGTITVTS 112
Qy 121 S 121
Db 113 A 113

RESULT 3

US-08-652-558-38
; Sequence 38, Application US/08652558
; Patent No. 5861155
; GENERAL INFORMATION:
; APPLICANT: LIN, AUGUSTINE YEE-THARN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF
; STREET: 75 STATE STREET, 23RD FLOOR
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,558
; FILING DATE: JUNE 6, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB94/00387
; FILING DATE: NOVEMBER 21, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, LEON R.
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,497-L
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-558-38

Query Match 84.3%; Score 535.5; DB 2; Length 120;
Best Local Similarity 86.0%; Pred. No. 5.9e-48;
Matches 104; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRVYGVHWVRQPPGKGLEWLGVWAGGSTNYN 60
Db 1 QVQLKESGPGLVAPSQSLITCTVSGFSLTAYGVNWVRQPPGKGLEWLGMWGDGNTDYN 60
Qy 61 SALMSRLSISKDNKSQVFLKMNLSQTDDTAMYYCARDRSTMITAYAMDYWGQGTITVTS 120
Db 61 SALKSRLSISKDNKSQVFLKMNLSQTDDTARYCARDRTV-ATLYAMDYWGQGTISVTVS 119
Qy 121 S 121
Db 120 S 120

RESULT 4
US-08-752-844-16
; Sequence 16, Application US/08752844
; Patent No. 5935821
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD

; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-09-293-533-16

Query Match 84.3%; Score 535; DB 4; Length 119;
Best Local Similarity 86.0%; Pred. No. 6.6e-48;
Matches 104; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHWRQPPGKGLEWLGVIWTGGSTNYN 60
|
Db 1 QVQLKESGPGLVAPSQSLITCTVSGFSLTSYGVHWRQPPGKGLEWLGVIWGDGSTNYN 60

QY 61 SALMSRLSISKDNKSQVFLKMNSLQTDTTAMYYCARDRSTMITAYAMDYWGQTTVTVS 120
|
Db 61 SALKSRLSISKDNKSQVFLKMNSLQTDTTARYYCAREXXX--XYIAMDYWGQTSVTVS 118

QY 121 S 121
|
Db 119 S 119

RESULT 7
US-08-943-136-4
; Sequence 4, Application US/08943136
; Patent No. 6291208
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; APPLICANT: Barber, Brian H
; APPLICANT: Cates, George A
; APPLICANT: Caterini, Judith E
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,136
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,576
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-733
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-943-136-4

Query Match 83.7%; Score 531.5; DB 3; Length 140;
Best Local Similarity 85.1%; Pred. No. 1.8e-47;
Matches 103; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

QY 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHWRQPPGKGLEWLGVIWTGGSTNYN 60
|
Db 21 QVQLKESGPGLVAPSQSLITCTVSGFSLTSYGVHWRQPPGKGLEWLGVIWAGGSINYN 80

QY 61 SALMSRLSISKDNKSQVFLKMNSLQTDTTAMYYCARDRSTMITAYAMDYWGQTTVTVS 120
|
Db 81 SALMSRLSISKDNFKSQVFLKMSSLQTDTTAMYYCARAYGDYV-HYAMDYWGQTSVTAS 139

QY 121 S 121
|
Db 140 S 140

RESULT 8
US-08-973-518-4
; Sequence 4, Application US/08973518
; Patent No. 6328962
; GENERAL INFORMATION:
; APPLICANT: Anand, Naveen N
; APPLICANT: Barber, Brian H
; APPLICANT: Cates, George A
; APPLICANT: Caterini, Judith E
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
; TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,518
; FILING DATE: 07-APR-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-973-518-4

Query Match 83.7%; Score 531.5; DB 3; Length 140;
Best Local Similarity 85.1%; Pred. No. 1.8e-47;
Matches 103; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

QY 1 QVQLQESGPGLVAPSQSLITCTVSGISLNRYGVHWRQPPGKGLEWLGVIWTGGSTNYN 60
|
Db 21 QVQLKESGPGLVAPSQSLITCTVSGFSLTSYGVHWRQPPGKGLEWLGVIWAGGSINYN 80

QY 61 SALMSRLSISKDNKSQVFLKMNSLQTDTTAMYYCARDRSTMITAYAMDYWGQTTVTVS 120
|
Db 81 SALMSRLSISKDNFKSQVFLKMSSLQTDTTAMYYCARAYGDYV-HYAMDYWGQTSVTAS 139

Qy 121 S 121
Db 140 S 140

RESULT 9
5455030-15
;Patent No. 5455030
; APPLICANT: LADNER, ROBERT C.;BIRD, ROBERT E.;HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPHY USING SINGLE CHAIN
;POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/40,440
; FILING DATE: 1-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
;SEQ ID NO:15:
; LENGTH: 242
5455030-15

Query Match 83.4%; Score 529.5; DB 6; Length 242;
Best Local Similarity 85.8%; Pred. No. 5.7e-47;
Matches 103; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

QY 2 VQLQESGPGVLVAPSQLSITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWGTGSTNYS 61
Db 124 VQLKESGPGVLVAPSQLSITCTVSGFSLTNYGVHVRQPPGKGLEWLGVIWAGNTNYS 183
QY 62 ALMSRLSISKDNKSQVFLKMNSLQDDTAMYYCARDRSTMITAYAMDYWGQTTVTSS 121
Db 184 ALMSRLSISKDNKSQVFLKMNSLQIDDTAIYYCAK-RLERIFYAMDYWGQTSVTSS 242

RESULT 10
US-08-881-037-67
; Sequence 67, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Glick, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Konski, Antoinette F.

; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-881-037-67

Query Match 82.8%; Score 525.5; DB 3; Length 121;
Best Local Similarity 86.0%; Pred. No. 6.4e-47;
Matches 104; Conservative 2; Mismatches 14; Indels 1; Gaps 1;
QY 1 QVQLQESGPGVLVAPSQLSITCTVSGISLNRYGVHVRQPPGKGLEWLGVIWGTGSTNYN 60
Db 1 QVQLLESGPVLVAPSQLSITCTVSGFSLTSYGVHVRQPPGKGLEWLGVIWAGGSTNYN 60
QY 61 SALMSRLSISKDNKSQVFLKMNSLQDDTAMYYCARDRS-TMITAYAMDYWGQTTVTV 119
Db 61 SALMSRLSISKDNKSQVFLKMNSLQDDTAMYYCAKHLPGYNGYYAMDYWGQTSVTV 120
QY 120 S 120
Db 121 S 121

RESULT 11
US-08-667-769A-15
; Sequence 15, Application US/08667769A
; Patent No. 5783184
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,769A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17082
; FILING DATE: 22-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-667-769A-15

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Query Match      82.4%; Score 523; DB 1; Length 119;
Best Local Similarity 82.6%; Pred. No. 1.1e-46;
Matches 100; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

      y      1  QVQLQESGPGLVAPSQSLSTICTVSGISLNRYGVHVRQPPGKGLEWLGVIWGGSTNYN 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      b      1  QVQLKESGPGLVAPSQSLSTICTVSGFSLTYSVHVRQPPGKGLEWLGVIWASGGTDYN 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

      y      61  SALMSRLSISKDNSKSOVFLKMNLSLQTDDTAMYYCARDSTRMTITAYAMDYWGQGTITVTS 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      b      61  SALMSRLSISKDNSKSOVFLKLNLSLQTDDTAMYYCARDPPSSL--LRLDYWGQGTITLTVS 118

      y      121  S 121
      |
      b      119  S 119

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RESULT 12
PCT-US95-17082A-15
; Sequence 15, Application PC/TUS9517082A
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17082A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-17082A-15

		Query Match	82.4%;	Score 523;	DB 5;	Length 119;	
		Best Local Similarity	82.6%;	Pred. No. 1.le-46;			
		Matches 100; Conservative	7;	Mismatches 12;	Indels	2;	Gaps 1
QY	1	QVQLQESGPGLVAPSQSLSICTVSGISLNRYGVHVRQP	PKGLEWLGVIWTGGSTNYN	60			
		:	:	:	:	:	:
Db	1	QVQLKESGPGLVAPSQSLSICTVSGFSLTSYSVHVRQP	PKGLEWLGVIWASGGTDYN	60			
		:	:	:	:	:	:
QY	61	SALMSRLSISKDNKSQVFELKMNSLQTDDTAMYYCARDSTRMITAYAMDYGQGTTVTVS	120				
		:	:	:	:	:	:
Db	61	SALMSRLSISKDNKSQVFELKLNSLQTDDTAMYYCARDPPSSL--LRLDYWGQGTTLTVS	118				
QY	121	\$ 121					
Db	119	\$ 119					

RESULT 13
US-09-189-129-3
; Sequence 3, Application US/09189129
; Patent No. 6323027
; GENERAL INFORMATION:
; APPLICANT: Burkly, Linda C
; APPLICANT: Benjamin, Christopher D
; APPLICANT: Hession, Catherine A
; APPLICANT: Whitty, Adrian
; TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/189,129
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: A006 PCT CIP
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 60/017,466
; FILING DATE: 10-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A006 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 679-2000
; TELEFAX: 617 679-2838
;

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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-189-129-3

Query Match      82.1%; Score 521.5; DB 3; Length 112;
Best Local Similarity 85.2%; Pred. No. 1.5e-46;
Matches 98; Conservative 8; Mismatches 6; Indels 3; Gaps 1;

QY 4 LOESGPGLVAPSQSLITCTVSGISLNPYGVHVRQPPGKGLEWLGVITWGGSTNYSAL 63
Db 1 LOESGPGLVAPSQSLITCTVSGFSLTSYGVHVRQPPGKGLEWLGVITWAGGSTNYSAL 60

QY 64 MSRLSISKDNKSQVFLKMNSLQTDTTAMYYCARDRSTMITAYAMDYWGQTTVT 118
Db 61 MSRLNINRDNSKQIFLKMNSLQTDTTAIYYCAREGSTV---DSMDYWGQTTVT 112

RESULT 14
US-09-824-286-3
; Sequence 3, Application US/09824286
; Patent No. 6770745
; GENERAL INFORMATION:
; APPLICANT: Burkly, Linda C
; Benjamin, Christopher D
; Hession, Catherine A
; Whitty, Adrian
; TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/824,286
; FILING DATE: 02-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,466
; FILING DATE: 10-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A006 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 679-2000
; TELEFAX: 617 679-2838
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-824-286-3
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Query Match 82.1%; Score 521.5; DB 4; Length 112;
Best Local Similarity 85.2%; Pred. No. 1.5e-46;

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Matches 98; Conservative 8; Mismatches 6; Indels 3; Gaps 1;

QY 4 LOESGPGLVAPSQSLITCTVSGISLNPYGVHVRQPPGKGLEWLGVITWGGSTNYSAL 63
Db 1 LOESGPGLVAPSQSLITCTVSGFSLTSYGVHVRQPPGKGLEWLGVITWAGGSTNYSAL 60

QY 64 MSRLSISKDNKSQVFLKMNSLQTDTTAMYYCARDRSTMITAYAMDYWGQTTVT 118
Db 61 MSRLNINRDNSKQIFLKMNSLQTDTTAIYYCAREGSTV---DSMDYWGQTTVT 112

RESULT 15
US-08-860-174A-2
; Sequence 2, Application US/08860174A
; Patent No. 5989830
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Paul James
; APPLICANT: VAN DER LOGT, Cornelis Paul Erik
; APPLICANT: VERHOEIJEN, Martine Elisa
; APPLICANT: WILSON, Steve
; TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
; TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; STREET: 9th Floor, East Tower
; CITY: WASHINGTON, D.C.
; STATE:
; COUNTRY: UNITED STATES
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text
; SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,174A
; FILING DATE: June 16, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95307332.7
; FILING DATE: October 16, 1995
; APPLICATION NUMBER: PCT/EP/96/03605
; FILING DATE: August 14, 1996
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-860-174A-2
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Query Match 81.5%; Score 517.5; DB 2; Length 239;
Best Local Similarity 82.6%; Pred. No. 9.8e-46;
Matches 100; Conservative 6; Mismatches 10; Indels 5; Gaps 1;

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QY 1 QVQLQESGPGLVAPSQSLITCTVSGISLNPYGVHVRQPPGKGLEWLGVITWGGSTNYN 60
Db 124 QVQLQESGPGLVAPSQSLITCTVSGFSLTGYGVNVRQPPGKGLEWLGMWGDGNTDYN 183

QY 61 SALMSRLSISKDNKSQVFLKMNSLQTDTTAMYYCARDRSTMITAYAMDYWGQTTVTVS 120
Db 184 SALKSRLSISKDNKSQVFLKMNSLHTDRTARYYCARERD-----YRLDYWGQTTVTVS 238

QY 121 S 121
Db 239 S 239
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 13, 2004, 13:12:35 ; Search time 21.6295 Seconds
(without alignments)
2201.453 Million cell updates/sec

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Perfect score: 674
Sequence: 1 gacattgagctcaccagtc.....gtatccatcttcaagttcc 359

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 956278

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	458	68.0	235	3	US-09-171-945-17
2	445	66.0	215	6	Sequence 17, Appl Patent No. 5455030-3
3	445	66.0	235	2	US-08-303-569B-5
4	445	66.0	235	2	Sequence 5, Appli
5	445	66.0	235	4	US-08-116-247-5
6	445	66.0	235	4	Sequence 5, Appli
7	444	65.9	235	4	US-09-795-515-5
8	444	65.9	255	3	Sequence 5, Appli
9	443.5	65.8	255	4	US-09-348-224-5
10	439	65.1	213	2	Sequence 8, Appli
11	427	63.4	256	4	US-09-553-498-8
12	427	63.4	258	4	Sequence 8, Appli
					Sequence 4, Appli
					Sequence 9, Appli
					Sequence 2, Appli
					Sequence 4, Appli

13	426	63.2	270	2	US-08-652-507-2	Sequence 2, Appli
14	426	63.2	553	2	US-08-661-052-16	Sequence 16, Appl
15	426	63.2	553	3	US-09-188-082-16	Sequence 16, Appl
16	426	63.2	553	3	US-09-364-088-16	Sequence 16, Appl
17	426	63.2	553	3	US-09-102-716-16	Sequence 16, Appl
18	425	63.1	223	2	US-08-190-199A-63	Sequence 63, Appl
19	425	63.1	235	3	US-09-423-439-58	Sequence 58, Appl
20	425	63.1	235	4	US-09-011-769A-23	Sequence 23, Appl
21	425	63.1	236	2	US-08-190-199A-65	Sequence 65, Appl
22	424	62.9	222	2	US-08-190-199A-67	Sequence 67, Appl
23	424	62.9	235	2	US-08-190-199A-61	Sequence 61, Appl
24	420	62.3	106	2	US-08-956-047-33	Sequence 33, Appl
25	420	62.3	128	2	US-08-956-047-31	Sequence 31, Appl
26	420	62.3	240	2	US-08-956-047-25	Sequence 25, Appl
27	420	62.3	281	3	US-09-423-439-44	Sequence 44, Appl
28	420	62.3	666	3	US-09-423-439-51	Sequence 51, Appl
29	417	61.9	108	4	US-09-948-004-28	Sequence 28, Appl
30	417	61.9	495	4	US-09-948-004-18	Sequence 18, Appl
31	414	61.4	103	1	US-08-467-393-4	Sequence 4, Appli
32	414	61.4	144	4	US-09-318-786-29	Sequence 29, Appl
33	413	61.3	129	2	US-08-116-778E-2	Sequence 2, Appli
34	413	61.3	129	2	US-08-438-562-2	Sequence 2, Appli
35	413	61.3	129	2	US-08-483-528B-92	Sequence 92, Appl
36	413	61.3	242	2	US-08-553-497A-28	Sequence 28, Appl
37	410.5	60.9	107	1	US-07-942-245-3	Sequence 3, Appli
38	409.5	60.8	110	3	US-08-836-561-33	Sequence 33, Appl
39	409.5	60.8	110	4	US-09-434-122-33	Sequence 33, Appl
40	409	60.7	106	3	US-08-397-411-9	Sequence 9, Appli
41	409	60.7	599	1	US-08-463-163-3	Sequence 3, Appli
42	408	60.5	100	2	US-08-308-494A-19	Sequence 19, Appl
43	408	60.5	106	1	US-07-634-278-1	Sequence 1, Appli
44	408	60.5	106	1	US-07-634-278-16	Sequence 16, Appl
45	408	60.5	106	1	US-08-477-728-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-171-945-17
; Sequence 17, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT FILING DATE: 1998-10-29
; PRIOR FILING DATE: 1997-02-14
; PRIOR FILING DATE: 1996-05-04
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-17

Alignment Scores:
Pred. No.: 8.33e-47
Score: 458.00
Percent Similarity: 83.76%
Best Local Similarity: 76.92%
Query Match: 67.95%
DB: 3
Length: 235
Matches: 90
Conservative: 8
Mismatches: 19
Indels: 0
Gaps: 0

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US-10-049-868A-1 (1-359) x US-09-171-945-17 (1-235)
QY      1  GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACC 60
Db      23  AspileGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 42
QY      61  ATGACCTGCAGTCCAGTTCAAGTGTTAATTACATGCACCTGGTTCAGCAGGAGTCGGGC 120
Db      43  ileThrCysSerAlaSerSerValThrTyrMetHisTrpPheGlnGlnLysProGly 62
QY      121  ACCTTCCCCAAAGAAGATTATATGACACATCCAAACTGGCTTCGGAGTCCCTGCTCGC 180
Db      63  ThrSerProLysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProAlaArg 82
QY      181  CTCAGTGGCAGTGGGTCTGGGACAGAAATTCACCCCTGGAAATCAGTAGACTGAAGGCTGAG 240
Db      83  PheSerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGlu 102
QY      241  GATGTGGGTGTGTATTACTGTCAACAACITGTAGAGTATCCGCTCACGTCACGTCGGTGGG 300
Db      103  AspAlaAlaThrTyrTyrCysGlnGlnArgSerThrTyrProLeuThrPheGlyAlaGly 122
QY      301  ACCAAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db      123  ThrLysLeuGluIleLysArgThrValAlaAlaProSerValPheIlePhe 139

RESULT 2
5455030-3
; Patent No. 5455030
; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
; POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/40,440
; FILING DATE: 1-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
; SEQ ID NO:3:
; LENGTH: 215
5455030-3

Alignment Scores:
Pred. No.:      3.01e-45      Length:      215
Score:          445.00      Matches:      90
Percent Similarity: 82.76%      Conservative: 6
Best Local Similarity: 77.59%      Mismatches: 18
Query Match:    66.02%      Indels:      2
DB:             6          Gaps:      1

US-10-049-868A-1 (1-359) x 5455030-3 (1-215)
QY      10  CTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGC 69
Db      4  LeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMetThrCys 23
QY      70  AGTCCAGTTCAAGTGT-----AATTACATGCACCTGGTTCAGCAGGAGTCGGGCACC 123
Db      24  ArgAlaSerSerSerValSerSerTyrLeuHisTrpPheGlnGlnLysSerGlyAla 43
QY      124  TTCCCCAAAGAAGGATTATATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db      44  SerProLysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProAlaArgPhe 63
QY      184  AGTGCAGTGGGTCTGGGACAGAAATTCACCCCTGGAAATCAGTAGAGTGAAGGCTGAGGAT 243

US-10-049-868A-1 (1-359) x US-08-303-569B-5 (1-235)
QY      4  ATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATG 63
Db      24  IleValLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43
QY      64  ACCTGCAGTGCCAGTTCAGTTCAAGTGTTAATTACATGCACCTGGTTCAGCAGGAGTCGGGCACC 123
Db      44  ThrCysSerAlaSerSerValSerTyrMetAsnTrpTyrGlnGlnLysSerGlyThr 63
QY      124  TTCCCCAAAGAAGGATTATATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db      64  SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaHisPhe 83

Db      64  SerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerValGluAlaAsp 83
QY      244  GTGGGTGTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCAGCTTCGGTGTGGGACC 303
Db      84  AlaAlaThrTyrTyrCysGlnGlnTyrSerGlyTyrProLeuThrPheGlyAlaGlyThr 103
QY      304  AAGCTGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db      104  LysLeuGluLeuLysArgAlaAspAlaAlaProIleValSerIlePhe 119

RESULT 3
US-08-303-569B-5
; Sequence 5, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,569B
; FILING DATE: 07-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-303-569B-5

Alignment Scores:
Pred. No.:      3.11e-45      Length:      235
Score:          445.00      Matches:      87
Percent Similarity: 83.62%      Conservative: 10
Best Local Similarity: 75.00%      Mismatches: 19
Query Match:    66.02%      Indels:      0
DB:             2          Gaps:      0
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QY 184 AGTGGCAGTGGGTCTGGACAGAATTCAACCCTGGAAATCAGTAGACTGAAGGCTGAGGAT 243
Db ||||||||||||||||||| :
84 ArgGlySerGlySerGlyThrSerTyrSerLeuThrIleSerGlyMetGluAlaGluAsp 103
QY 244 GTGGGTGTATTACTGTCAACAACCTGTAGAGTATCCGCTCAGCTCGGTGCTGGGACC 303
Db ||||||||||||||||||| :
104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProPheThrPheGlySerGlyThr 123
QY 304 AAGCTGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db ||||||||||| :
124 LysLeuGluIleAsnArgAlaAspThrAlaProThrValSerIlePhe 139

RESULT 4

US-08-116-247-5
; Sequence 5, Application US/08116247
; Patent No. 5929212
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5929212ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,247
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paintin, Francis A.
; REGISTRATION NUMBER: 19,386
; REFERENCE/DOCKET NUMBER: CARP-0011
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-116-247-5

Alignment Scores:
Pred. No.: 3.11e-45 Length: 235
Score: 445.00 Matches: 87
Percent Similarity: 83.62% Conservative: 10
Best Local Similarity: 75.00% Mismatches: 19
Query Match: 66.02% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x US-08-116-247-5 (1-235)

QY 4 ATTGAGCTCACCCAGTCTCCAGCAATCATGTGTCATCTCCAGGGGAGAAGGTCAACCATG 63
Db ||| |||||||ThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43
QY 64 ACCTGCAGTGCAGTTCAGTGTTAATTACATGCACTGGTTCCAGCAGGAGTGGGCACC 123

Db 44 ThrCysSerAlaSerSerSerValSerTyrMetAsnTrpTyrGlnGlnLysSerGlyThr 63
QY 124 TTCCCAAAAAGAGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db ||||||||||| ||||||| :
64 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaHisPhe 83
QY 184 AGTGCAGTGGGTCTGGGACAGAATTCAACCCTGGAAATCAGTAGAGTGAAGGCTGAGGAT 243
Db ||||||||||| :
84 ArgGlySerGlySerGlyThrSerTyrSerLeuThrIleSerGlyMetGluAlaGluAsp 103
QY 244 GTGGGTGTATTACTGTCAACAACCTGTAGAGTATCCGCTCAGCTCGGTGCTGGGACC 303
Db ||||||||||| :
104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProPheThrPheGlySerGlyThr 123
QY 304 AAGCTGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db ||||||||||| :
124 LysLeuGluIleAsnArgAlaAspThrAlaProThrValSerIlePhe 139

RESULT 5

US-09-795-515-5
; Sequence 5, Application US/09795515
; Patent No. 6632927
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6632927ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-795-515-5

Alignment Scores:
Pred. No.: 3.11e-45 Length: 235
Score: 445.00 Matches: 87
Percent Similarity: 83.62% Conservative: 10
Best Local Similarity: 75.00% Mismatches: 19
Query Match: 66.02% Indels: 0
DB: 4 Gaps: 0

US-10-049-868A-1 (1-359) x US-09-795-515-5 (1-235)

QY 4 ATTGAGCTACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCCACCATG 63
Db 24 IlevallLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43
QY 64 ACCTGCAGTGCCAGTTCAAGTGTTAATTACATGCACCTGGTTCCAGCAGGAGTCGGGCACC 123
Db 44 ThrCysSerAlaSerSerValSerTyrMetAsnTrpTyrGlnGlnLysSerGlyThr 63
QY 124 TTCCCCAAAAGAGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db 64 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaHisPhe 83
QY 184 AGTGGCAGTGGTCTGGGACAGAAATTCACCTCGAAATCAGTAGAGTGAGGCTGAGGAT 243
Db 84 ArgGlySerGlySerGlyThrSerTyrSerLysLeuThrIleSerGlyMetGluAlaGluAsp 103
QY 244 GTGGGTGTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTTCGGTGTGGGACC 303
Db 104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProPheThrPheGlySerGlyThr 123
QY 304 AAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db 124 LysLeuGluIleAsnArgAlaAspThrAlaProThrValSerIlePhe 139

RESULT 6

US-09-348-224-5
; Sequence 5, Application US/09348224
; Patent No. 6750325

GENERAL INFORMATION:
; APPLICANT: Jollieffe, Linda Kay
; APPLICANT: Zivin, Robert Allan

APPLICANT: Adair, John Robert
; APPLICANT: Athwal, Diljeet Singh

TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; FILE REFERENCE: CARP0066

CURRENT APPLICATION NUMBER: US/09/348,224
; CURRENT FILING DATE: 1999-07-06

EARLIER APPLICATION NUMBER: 08/116,247
; EARLIER FILING DATE: 1993-09-03

EARLIER APPLICATION NUMBER: 07/743,377
; EARLIER FILING DATE: 1991-10-04

NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 5
; LENGTH: 235

TYPE: PRT
; ORGANISM: Mouse

US-09-348-224-5

Alignment Scores:
Pred. No.: 3.11e-45 Length: 235
Score: 445.00 Matches: 87
Percent Similarity: 83.62% Conservative: 10
Best Local Similarity: 75.00% Mismatches: 19
Query Match: 66.02% Indels: 0
DB: 4 Gaps: 0

US-10-049-868A-1 (1-359) x US-09-348-224-5 (1-235)

QY 4 ATTGAGCTACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCCACCATG 63
Db 24 IlevallLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrMet 43
QY 64 ACCTGCAGTGCCAGTTCAAGTGTTAATTACATGCACCTGGTTCCAGCAGGAGTCGGGCACC 123
Db 44 ThrCysSerAlaSerSerValSerTyrMetAsnTrpTyrGlnGlnLysSerGlyThr 63
QY 124 TTCCCCAAAAGAGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTC 183
Db 64 SerProLysArgTrpIleTyrAspThrSerLysLeuAlaSerGlyValProAlaHisPhe 83
QY 184 AGTGGCAGTGGTCTGGGACAGAAATTCACCTCGAAATCAGTAGAGTGAGGCTGAGGAT 243

Db 84 ArgGlySerGlySerGlyThrSerTyrSerLeuThrIleSerGlyMetGluAlaGluAsp 103
QY 244 GTGGGTGTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTCCGGTGTGGACC 303
Db 104 AlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProPheThrPheGlySerGlyThr 123
QY 304 AAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db 124 LysLeuGluIleAsnArgAlaAspThrAlaProThrValSerIlePhe 139

RESULT 7

US-09-553-498-8

; Sequence 8, Application US/09553498
; Patent No. 6309861

GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee

APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg

APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: Process for the production of naturally folded and secreted prot

FILE REFERENCE: Case 20379
; CURRENT APPLICATION NUMBER: US/09/553,498

CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: EP99107412.1

PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 10

SEQ ID NO 8
; LENGTH: 255

TYPE: PRT
; ORGANISM: E. coli

US-09-553-498-8

Alignment Scores:

Pred. No.: 4.24e-45 Length: 255
Score: 444.00 Matches: 88
Percent Similarity: 86.36% Conservative: 7
Best Local Similarity: 80.00% Mismatches: 15
Query Match: 65.88% Indels: 0
DB: 3 Gaps: 0

US-10-049-868A-1 (1-359) x US-09-553-498-8 (1-255)

QY 1 GACATTGAGTCAACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCCACC 60
Db 132 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 151
QY 61 ATGACCTGCAGTCCCAGTCAAGTGTAAATTACATGCACCTGGTTCCAGCAGGAGTCGGGC 120
Db 152 MetThrCysSerAlaSerSerValArgTyrMetAsnTrpPheGlnGlnLysSerGly 171
QY 121 ACCTTCCCCAAAAGAGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 172 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuSerSerGlyValProAlaArg 191
QY 181 CTCAGTGGCAGTGGGTCTGGGACAGAAATTCACCTCGAAATCAGTAGAGTGAAGGCTGAG 240
Db 192 PheSerGlySerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 211
QY 241 GATGTGGGTGTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTCCGGTGTGGG 300
Db 212 AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 231
QY 301 ACCAAGCTGGAGCTGAAACGGGCTGATGCT 330
Db 232 ThrLysLeuGluLeuLysArgAlaAlaAla 241

RESULT 8

US-09-618-869-8

; Sequence 8, Application US/09618869
; Patent No. 6455279

GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee

APPLICANT: Rudolph, Rainer


```
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND
; TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
; TITLE OF INVENTION: CHAPERONES
; FILE REFERENCE: 20381
; CURRENT APPLICATION NUMBER: US/09/618,869
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: EP99114811.5
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-618-869-8

Alignment Scores:
Pred. No.: 4.24e-45 Length: 255
Score: 444.00 Matches: 88
Percent Similarity: 86.36% Conservative: 7
Best Local Similarity: 80.00% Mismatches: 15
Query Match: 65.88% Indels: 0
DB: 4 Gaps: 0

US-10-049-868A-1 (1-359) x US-09-618-869-8 (1-255)

QY 1 GACATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCACC 60
Db 132 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluIysValThr 151

QY 61 ATGACCTGCAGTCCAGTTCAGGTGTTAATTACATGCACCTGGTTCAGCAGGAGTCGGGC 120
Db 152 MetThrCysSerAlaSerSerValArgTyrMetAsnTrpPheGlnGlnLysSerGly 171

QY 121 ACCTTCCCCAAAGAGGATTATGACACATCCAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 172 ThrSerProLysArgTrpIleTyrAspThrSerLysLeuSerSerGlyValProAlaArg 191

QY 181 CTCAGTGGCAGTGGGTCTGGGACAGAAATTCACCCCTGGAAATCAGTAGAGTGAGGCTGAG 240
Db 192 PheSerGlySerGlyThrSerTyrSerLeuThrIleSerSerMetGluAlaGlu 211

QY 241 GATGTGGGTGTGTATTACTGTCAACAACCTGTAGAGTATCCGCTCACGTTCCGCTGGG 300
Db 212 AspAlaAlaThrTyrTyrCysGlnGlnTrpSerSerAsnProLeuThrPheGlyAlaGly 231

QY 301 ACCAAGCTGGAGCTGAAACGGGCTGATGCT 330
Db 232 ThrLysLeuGluLeuLysArgAlaAlaAla 241

RESULT 9
US-08-737-129A-4
; Sequence 4, Application US/08737129A
; Patent No. 585816
; GENERAL INFORMATION:
; APPLICANT: Ikuo FUJII et al.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
; TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,129A
; FILING DATE: No. 585816member 15, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-737-129A-4

Alignment Scores:
Pred. No.: 4.56e-45 Length: 213
Score: 443.50 Matches: 86
Percent Similarity: 83.76% Conservative: 12
Best Local Similarity: 73.50% Mismatches: 18
Query Match: 65.80% Indels: 1
DB: 2 Gaps: 1

US-10-049-868A-1 (1-359) x US-08-737-129A-4 (1-213)

QY 1 GACATTGAGCTCACCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGTCACC 60
Db 1 GluLeuValMetThrGlnThrProAlaIleMetSerAlaSerProGlyGluIysValThr 20

QY 61 ATGACCTGCAGTCCAGTTCAGGTGTTAATTACATGCACCTGGTTCAGCAGGAGTCGGGC 120
Db 21 MetThrCysSerAlaSerSerIleSerTyrMetHisTrpTyrGlnGlnLysProGly 40

QY 121 ACCTTCCCCAAAGAGGATTATGACACATCCAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 41 ThrProProLysArgTrpIleTyrGlyThrSerLysLeuThrSerGlyValProAlaArg 60

QY 181 CTCAGTGGCAGTGGGTCTGGGACAGAAATTCACCCCTGGAAATCAGTAGAGTGAGGCTGAG 240
Db 61 PheSerGlySerGlySerGlyThrSerPheSerLeuThrIleSerSerMetGluAlaGlu 80

QY 241 GATGTGGGTGTGTATTACTGTCAACAACCTGTAGAGTATCCGCTCACGTTCCGCTGGG 300
Db 81 AspAlaAlaThrTyrTyrCysHisGlnArgSerSerTyrPro---ThrPheGlyGlyGly 99

QY 301 ACCAAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 351
Db 100 ThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSerIlePhe 116

RESULT 10
US-09-171-945-9
; Sequence 9, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
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; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-9

Alignment Scores:
Pred. No.: 1.25e-44 Length: 108
Score: 439.00 Matches: 86
Percent Similarity: 85.19% Conservative: 6
Best Local Similarity: 79.63% Mismatches: 16
Query Match: 65.13% Indels: 0
DB: 3 Gaps: 0

US-10-049-868A-1 (1-359) x US-09-171-945-9 (1-108)

QY 1 GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAAGGTCACC 60
Db 1 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 20

QY 61 ATGACCTGCAGTCCAGTTCAAAGTGTAAATTACATGCACTGGTTCACGAGGATCGGGC 120
Db 21 IleThrCysSerAlaSerSerValThrTyrMetHisTrpPheGlnGlnLysProGly 40

QY 121 ACCTTCCCCAAAGAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 41 ThrSerProLysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProAlaArg 60

QY 181 CTCAGTGGCAGTGGGTCTGGGACAGAAATTCACCCCTGGAATCAGTAGAGTGAAGGCTGAG 240
Db 61 PheSerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGlu 80

QY 241 GATGTGGGTGTGTATTACTGTCAACAACCTGTAGAGTATCCGCTCACGTTCCGCTGGG 300
Db 81 AspAlaAlaThrTyrTyrCysGlnGlnArgSerThrTyrProLeuThrPheGlyAlaGly 100

QY 301 ACCAAGCTGGAGCTGAAACGGGCT 324
Db 101 ThrLysLeuGluLeuLysArgAla 108

RESULT 11
US-09-526-738A-2
; Sequence 2, Application US/09526738A
; Patent No. 6630584
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
; APPLICANT: LTD.
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336
; CURRENT APPLICATION NUMBER: US/09/526,738A
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Humanus
US-09-526-738A-2

Alignment Scores:
Pred. No.: 4.83e-43 Length: 256
Score: 427.00 Matches: 84
Percent Similarity: 80.70% Conservative: 8
Best Local Similarity: 73.68% Mismatches: 22
Query Match: 63.35% Indels: 0
DB: 4 Gaps: 0

DB: 4 Gaps: 0
US-10-049-868A-1 (1-359) x US-09-526-738A-2 (1-256)

QY 1 GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAAGGTCACC 60
Db 132 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 151

QY 61 ATGACCTGCAGTCCAGTTCAAAGTGTAAATTACATGCACTGGTTCACGAGGATCGGGC 120
Db 152 IleThrCysSerAlaSerSerValAsnTyrMetHisTrpPheGlnGlnLysProGly 171

QY 121 ACCTTCCCCAAAGAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 172 ThrSerProLysLeuTrpIleSerSerThrSerAsnLeuAlaSerGlyValProAlaArg 191

QY 181 CTCAGTGGCAGTGGGTCTGGGACAGAAATTCACCCCTGGAATCAGTAGAGTGAAGGCTGAG 240
Db 192 PheSerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGlu 211

QY 241 GATGTGGGTGTGTATTACTGTCAACAACCTGTAGAGTATCCGCTCACGTTCCGCTGGG 300
Db 212 AspAlaAlaThrTyrTyrCysGlnGlnArgSerSerTyrProTyrThrPheGlyGlyGly 231

QY 301 ACCAAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTA 342
Db 232 ThrLysLeuGlnIleLysArgAlaAlaAlaGlyAlaProVal 245

RESULT 12
US-09-526-738A-4
; Sequence 4, Application US/09526738A
; Patent No. 6630584
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
; APPLICANT: LTD.
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336
; CURRENT APPLICATION NUMBER: US/09/526,738A
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Humanus
US-09-526-738A-4

Alignment Scores:
Pred. No.: 4.84e-43 Length: 258
Score: 427.00 Matches: 84
Percent Similarity: 80.70% Conservative: 8
Best Local Similarity: 73.68% Mismatches: 22
Query Match: 63.35% Indels: 0
DB: 4 Gaps: 0

US-10-049-868A-1 (1-359) x US-09-526-738A-4 (1-258)

QY 1 GACATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAAGGTCACC 60
Db 134 AspIleGluLeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThr 153

QY 61 ATGACCTGCAGTCCAGTTCAAAGTGTAAATTACATGCACTGGTTCACGAGGATCGGGC 120
Db 154 IleThrCysSerAlaSerSerValAsnTyrMetHisTrpPheGlnGlnLysProGly 173

QY 121 ACCTTCCCCAAAGAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGC 180
Db 174 ThrSerProLysLeuTrpIleSerSerThrSerAsnLeuAlaSerGlyValProAlaArg 193

QY 181 CTCAGTGGCAGTGGGTCTGGGACAGAAATTCACCCCTGGAATCAGTAGAGTGAAGGCTGAG 240
Db 194 PheSerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGlu 213

QY 241 GATGTGGGTGTATTACTGTCAACAACCTGTAGAGTATCCGCTCAGGTTTCGGTGGG 300
Db 214 AspAlaAlaThrTyrCysGlnGlnArgSerSerTyrProTyrThrPheGlyGlyGly 233
QY 301 ACCAAGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTA 342
Db 234 ThrLysLeuGlnIleLysArgAlaAlaAlaGlyAlaProVal 247

RESULT 13
US-08-652-507-2
; Sequence 2, Application US/08652507
; Patent No. 5876691
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye, P.C.
; STREET: 1100 No. 5876691th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,507
; FILING DATE: 02-Jul-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Arthur R. Crawford
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 117-211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-507-2

Alignment Scores:
Pred. No.: 6.5e-43 Length: 270
Score: 426.00 Matches: 83
Percent Similarity: 85.71% Conservative: 7
Best Local Similarity: 79.05% Mismatches: 15
Query Match: 63.20% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x US-08-652-507-2 (1-270)

QY 10 CTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGC 69
Db 165 LeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrIleThrCys 184
QY 70 AGTGCCAGTTCAAGTGTAAATTACATGCACCTGGTTCCAGCAGGAGTCGGGCACCTTCCCC 129
Db 185 SerAlaSerSerSerValSerTyrMetHisTrpPheGlnGlnLysProGlyThrSerPro 204
QY 130 AAAAGAAGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTCAGTGGC 189
Db 205 LysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProAlaArgPheSerGly 224
QY 190 AGTGGGTCTGGGACAGAATTCACCCCTGGAAATCAGTAGAGTGAAGGCTCAGGATGTGGGT 249
Db 225 SerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGluAspAlaAla 244

QY 250 GTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCAGGTTTCGGTGGGACCAAGCTG 309
Db 245 ThrTyrTyrCysGlnGlnArgSerSerTyrProLeuThrPheGlyAlaGlyThrLysLeu 264
QY 310 GAGCTGAAACGGGCT 324
Db 265 GluLeuLysArgAla 269
RESULT 14
US-08-661-052-16
; Sequence 16, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-Fc RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-661-052-16

Alignment Scores:
Pred. No.: 8.44e-43 Length: 553
Score: 426.00 Matches: 83
Percent Similarity: 85.71% Conservative: 7
Best Local Similarity: 79.05% Mismatches: 15
Query Match: 63.20% Indels: 0
DB: 2 Gaps: 0

US-10-049-868A-1 (1-359) x US-08-661-052-16 (1-553)

QY 10 CTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCTGC 69
Db 415 LeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrIleThrCys 434
QY 70 AGTGCCAGTTCAAGTGTAAATTACATGCACCTGGTTCCAGCAGGAGTCGGGCACCTTCCCC 129
Db 435 SerAlaSerSerSerValSerTyrMetHisTrpPheGlnGlnLysProGlyThrSerPro 454
QY 130 AAAAGAAGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTCAGTGGC 189

Db

455

LysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProAlaArgPheSerGly

474

QY

190

AGTGGGCTCTGGACAGAAATTCACCCCTGGAATCAGTAGAGTGAAGGCTGAGGATGTGGGT

249

Db

475

SerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGluAspAlaAla

494

QY

250

GTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTTCGGTGGTGGGACCAAGCTG

309

Db

495

ThrTyrTyrCysGlnGlnArgSerSerTyrProLeuThrPheGlyAlaGlyThrLysLeu

514

QY

310

GAGCTGAAACGGGCT

324

Db

515

GluLeuLysArgAla

519

RESULT 15

US-09-188-082-16

/ Sequence 16, Application US/09188082

/ Patent No. 6270765

/ GENERAL INFORMATION:

/ APPLICANT: Yashwant M. Deo

/ APPLICANT: Joel Goldstein

/ APPLICANT: Robert Graziano

/ APPLICANT: Chezian Somasundaram

/ TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED

/ TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES

/ NUMBER OF SEQUENCES: 16

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: LAHIVE & COCKFIELD

/ STREET: 60 State Street, Suite 510

/ CITY: Boston

/ STATE: Massachusetts

/ COUNTRY: USA

/ ZIP: 02109-1875

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: PatentIn Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/188,082

/ FILING DATE:

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: 08/661,052

/ FILING DATE:

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Arnold, Beth E.

/ REGISTRATION NUMBER: 35,430

/ REFERENCE/DOCKET NUMBER: MXI-043CP

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (617)227-7400

/ TELEFAX: (617)227-5941

/ INFORMATION FOR SEQ ID NO: 16:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 553 amino acids

/ TYPE: amino acid

/ TOPOLOGY: linear

/ MOLECULE TYPE: protein

US-09-188-082-16

Alignment Scores:

Pred. No.: 8.44e-43 Length: 553

Score: 426.00 Matches: 83

Percent Similarity: 85.71% Conservative: 7

Best Local Similarity: 79.05% Mismatches: 15

Query Match: 63.20% Indels: 0

DB: 3 Gaps: 0

US-10-049-868A-1 (1-359) x US-09-188-082-16 (1-553)

QY

10

CTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGGTCACCATGACCTGC

69

Db

415

LeuThrGlnSerProAlaIleMetSerAlaSerProGlyGluLysValThrIleThrCys

434

QY

70

AGTGCCAGTTCAAAGTGTTAATTACATGCAGCTGGTTCAGCAGGAGTCGGGCACCTTCCCC

129

Db

435

SerAlaSerSerSerValSerTyrMetHisTrpPheGlnGlnLysProGlyThrSerPro

454

QY

130

AAAAGAAGGATTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCCTCAGTGGC

189

Db

455

LysLeuTrpIleTyrSerThrSerAsnLeuAlaSerGlyValProAlaArgPheSerGly

474

QY

190

AGTGGGTCCTGGACAGAAATTCACCCCTGGAATCAGTAGAGTGAAGGCTGAGGATGTGGGT

249

Db

475

SerGlySerGlyThrSerTyrSerLeuThrIleSerArgMetGluAlaGluAspAlaAla

494

QY

250

GTGTATTACTGTCAACAACCTTGTAGAGTATCCGCTCACGTTTCGGTGGTGGGACCAAGCTG

309

Db

495

ThrTyrTyrCysGlnGlnArgSerSerTyrProLeuThrPheGlyAlaGlyThrLysLeu

514

QY

310

GAGCTGAAACGGGCT

324

Db

515

GluLeuLysArgAla

519

Search completed: October 13, 2004, 13:31:11

Job time : 24.6295 secs